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July 29, 2002, 15:57:10; Search time 70.63 Seconds (without alignments) 55.779 Million cell updates/sec
                                                                                                                                                                         US-09-641-104A-6
204
1 HREGLLAIFKSGGIPALVKM......GSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                                                                              283138
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      283138 seqs, 96089334 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	į	1	C		plakoglobin, desmo plakoglobin - Afri	armadillo segment	hypothetical prote		beta-catenin - Hyd	beta-catenin - Cae	probable importin	SRP1 protein homol	probable nuclear t	arm repeat contain	hypothetical prote	hypothetical prote	armadillo protein	VAC8 protein - yea	hypothetical prote	probable nuclear t	hypothetical prote	3-deoxy-D-manno-oc	probable membrane	importin alpha - t	hypothetical prote	conserved hypothet	conserved hypothet	hypothetical prote
SUMMARIES 3 ID	\$ \$35099	2 A38973	2 S35091	2 335092 3 323005	2 S35093	2 T12689	2, S33793	2 S33794	2 JC4835	2 T23341	2 A86157	2 T01516	2 T52099	2 T45588	2 AF2163	2 T06735	2 T43175	2 S50446	2 T48204	2 T52101	2 F86225	2 E83023	2 S34929	2 T04329	2 T06629	2 AD1432	2 AD1433	2 B86150
% Query Match Length DB		100.0 781 2	100.00		2.79	92.2 843 2		. 7		51.0 678 2	31.9 538 2						28.9 811 2			27.9 528 2					27.0 402 2		0.	27.0 571 2
Result No. Score	1 204	2 204	3 204		9	7 188	8 184	6 179	10 160	1. 1.	17 65	13	14	15	16	17 5	18 59	85 6I B			22 57				26 55	55 72 F	28 55	Y 29 25

	cell division prot	hypothetical prote	sodium/alanine sym	gene p120 protein	hypothetical prote	probable 3-isoprop	hypothetical prote	neural plakophilin	hypothetical prote	conserved hypothet	ciliary neurotroph	hypothetical prote	DNA helicase Q1 in	nuclear localizati	pendulin - mouse	m-importin (nuclea
	T06774	T40294	н82200	S28498	F97844	E71180	T26395	T42209	B70083	E69218	I58141	D72638	JC5505	A56516	S57873	S57345
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	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT: 1: 535099 :: 535099 :: 535099 :: 535099 :: 61	A; Residues: 1-781 <hue> A; Residues: 1-781 <hue> A; Cross-references: GB:219054; NID:g38519; PIDN:CAA79497.1; PID:g38520 A; Cross-references: GB:219054; NID:g38519; PIDN:CAA79497.1; PID:g38520 A; Rollet, F.; Berx, G.; Molemans, F.; van Roy, F. submitted to the EMBL Data Library, June 1995 A; Description: H. sapiens beta-catenin mRNA. A; Reference number: 553356 A; Accession: 55336 A; Accession: 55336 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-781 <nol> A; Residues: 1-781 <nol> A; Cross-references: EMBL:X87838; NID:g1154853; PIDN:CAA61107.1; PID:g860988 C; Comment: The cytoplasmic protein beta-catenin normally binds to a region in the cyt</nol></nol></hue></hue>
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plakoglobin - African clawed frog clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S35093; S24636
R;Fouquet, B: Zimbelmann, R:; Franke, W.W.
Differentiation 51, 187-194, 1992
A;Title: Identification of plakoglobin in oocytes and early embryos of Xenopus laevis
A;Reference number: S35093; MUID:93093332
                                                                                          C; Species; ; Homo sapiens (man)
C; Species; ; Homo sapiens (man)
C; Date: -22, Nov-1089; Rsequence_revision 22-Nov-1989 #text_change 29-Aug-1997
C; Accession: A32905:
R; Franke; 'W.W.; Goldschmidt; M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cow Proc. Natl; Acad. Scl., U.S.A. 86, 4027-4031, 1989
A; Tille: Molecular cloning and amino acid sequence of human plakoglobin, the common j A; Reference number: A32905; MUID:89264555
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R;Demarais, A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 133-184, 'V',186-225,'T',227-292 <DEM>
A;Cross-references: EMBL:X67078; NID:g65252; PID:g65253
C;Reywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 HREGILAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 HREGLLSIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLL 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 191; DB 2;
Pred. No. 1.2e-17;
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Pred. No. 3e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            OMIM: 173325
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cy. 90.28;
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92.78;
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                                                                   - human
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Best Local Similarity 92.7
Matches 38; Conservative
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C; Keywords: cytoskeleton
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Best Local Similarity 9
Matches 37
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A;Molecule:type: mRNA
A;Residues: 1-738 <FOU>
                                                                     plakoglobin, desmosomal
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                                                                                                                                                                                                                                                                                           A; Status: preliminary A; Molecule type: mRNA
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                    RESULT
A32905
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                       Comment: Cellular levels of beta-catenin are regulated in part by the adenomatous poly
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S35092
R;Butz, S.; Stappert, J.; Weissig, H.; Kemler, R.
Science 257, 1142-1144, 1992
A;Title: Plakoglobin and beta-catenin: distinct but closely related.
A;Reference number: S35091; MUID:92376536
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-621 - PUTTY- NACCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-781 < SUUT>
A, Cross-references: EMBL:M90364; NID:g192141; PIDN:AAA37280.1; PID:g192142
C; Keywords: cytoskeleton
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R; Butz, S.; Stappert, J.; Weissig, H.; Kemler, R.
Science 257, 1142-1144, 1992
A; Title: Plakoglobin and beta-catenin: distinct but closely related.
A; Reference number: S35091; MUID:92376536
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                                                                                          A/Gene: GDB:CTNNB1; CTNNB
A/Cross-references: GDB:141922; OMIM:116806
A/Map position: 3P22-3P21.3
C/Reywords: apoptosis; carcinogenesis; cell adhesion; cytosol
F;151-676/Region: 40-residue repeats
                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                              2.2e-19;
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100.0%; Pred. No. 2.2e-19;
iive 0; Mismatches 0;
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Pred. No. 9.8e-18;
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92.7%;
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C;Keywords: cytoskeleton
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 41; Conservative
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Best Local Similarity
Matches 41; Conserv
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Best Local Similarity
Matches 38; Conserv
                                              cancerous cell growth.
microfilament network.
C;Comment: Cellular le
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Gaps

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A; Molecule type: mRNA
A; Residues: 1-820 <ROS>
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C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C; Accession: 833793
R; Rosenthal, E.
Biochim. Biophys. Acta 1173, 337-341, 1993
A; Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver A; Reference number: 833793; MUID:93305730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein - sea urchin (Tripneustes gratilla)
C.Species: Tripneustes gratilla
C.Jate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C.Accession: 833794
R.Rosenthal, E.
Biochim. Biophys. Acta 1173, 337-341, 1993
A.Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver
                                                                                                                                                                                                                                                                                                                          an
                                                                                                                                                                                           A; Residues: 1-843 <FER>
A; Residues: 1-843 <FER>
A; Cross-references: BMBL:AL021106; NID:e1371406; PID:e1249776; PIDN:CAA15946.1
A; Experimental source: clone cosmid 63B12
A; Experimental source: clone cosmid 63B12
B; Riggleman, B.; Wieschaus, E.; Schedl, P.
R; Riggleman, B.; Wieschaus, B.; Schedl, Muld. B99211895
A; Reference number: A31861; Muld. B99211895
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                      R.Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G. submitted to the EMBL Data Library, January 1998
A.Description: Sequencing the distal X chromosome of Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-843 <RIG>
A;Cross-references: EMBL:X54468; NID:g7610; PIDN:CAA38350.1; PID:g7611
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Pred. No. 1.2e-16;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 188; DB 2;
Pred. No. 3.4e-17;
3; Mismatches
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                                                                                                                A;Accession: T12689
A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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A;Introns: 11/1; 557/3; 624/3; 715/3; 748/1
A;Note: 86E4.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%; Scc.
87.8%; Pred
3;
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90.2%;
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Best Local Similarity 90.2
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
C; Accession: T12689; A31861
                                                                                                 Reference number: 217572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
`~hes 36; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: %b&4.v
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-817 <ROS>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A31861
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beta-catenin - Hydra magnipapillata
C;Species: Hydra magnipapillata
C;Saccession: JG4835
R;Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T.
Gene 172, 155-159, 1996
A;Title: Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadill
A;Reference number: JG4835; MUID:96257271
A;Reference number: JG4835
A;Status: nucleic acid sequence not shown
A;Residues: 1-806 < HOBS
A;Cross-treferences: GB:U36781; NID:91407600; PIDN:AAC47137.1; PID:91407601
C;Goment: This protein plays roles in cadherin-mediated cell adhesion and in signal
C;Genetics:
A;Gene: betaCtn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deta-catenin - Caenorhabditis elegans
C.Species: T5-oct-1999 #sequence_revision 15-oct-1999 #text_change 31-Jan-2000
C.Accession: T23341, T42221
R.Harris, B.
Submitted to the EMBL Data Library, November 1996
A.Accession: T23341
A.Scession: T23341
A.Scession: T23341
A.Scession: T23341
A.Secssion: T23341
A.Molecule: type: DNA
A.Residues: 1-678 <WIL>
A.Molecule: type: DNA
A.Residues: 1-678 <WIL>
A.Molecule: type: DNA
A.Residues: 1-678 <WIL>
A.Molecule: type: DNA
A.Residues: 22085
A.Accession: T42221
A.Accession: T42221
A.Accession: T42221
A.Accession: T42221
A.Molecule: type: mRNA
A.Residues: 1-678 <COS>
A.Residues: 1-678 <COS
A.Residues: 1-678 <COS
A.Residues: 1-678 <CO
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                                                                                                   Gaps
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             Length
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         Score 179; DB 2;
Pred. No. 5.5e-16;
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Pred. No. 2e-13;
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                                                                                              3; Mismatches
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87.7%;
ilarity 85.4%;
Conservative
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Best Local Similarity .73.2%;
Matches 30; Conservative
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A;Map position: 1
Query Match
Best Local Similarity
Matchés 35; Conserv
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DB 2;

51.0%; Score 104;

44.4

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probable inclear transport factor importin alpha [imported] - Arabidopsis thallana probable inclear transport factor importin alpha [imported] - Arabidopsis thaliana (mouse ear cress) C.Species: Arabidopsis thaliana (mouse ear cress) C.Species: $2000 **sequence_revision 20-0ct-2000 **text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T45588 R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, submittée to the Protein Sequence Database, December 1999 A;Reference number: Z23008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: protein F12A12.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04*Feb-2000 #sequence_revision 04*Feb-2000 #text_change 04*Feb-2000
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A.Residues: 1-660 <CHO>
A.Gross-references: EMBL:AL133314
A.Experimental source: cultivar Columbia; BAC clone Fl2A12
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Pred. No. 1.2;
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                                                                                                                                                                                                                                 C. Accessión: T52099: 4. ...
R. Schledž'ým.; Leclèrc'íD.; Neuhaus, G.; Merkle,
submittég; to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                              A;Residues; 1-531 <SCH>
A;Cross-references: EMBL:Y15225; PIDN:CAA75514.1
A;Experimental source: ecotype Columbia DESCR
C;Genetics:
282 AVIEAGVVPRLIQLLGHSSPSVLIPALRTIGNIV 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 1.2; 11; Mismatches
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Pred. No.
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Best Local Similarity 35.3%;
Matches 12; Conservative 1.
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Best Local Similarity, 38.2%;
Matches: 13; Conservative
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A,Introns: 90/3; 129/3; 279/3
A,Note: F12A12.30
                                                                                                                                                                                                                                                                                                 A; Reference number: 225953
A; Accession: T52099
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C;Superfamily: pendulin
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                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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                                                                                                                                                                                                                                                        probable importin alpha subunit [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001
C;Accession: A8615;
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ransen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A86157
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R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
Martienssen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
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A; Residues: 1-531 < JOH>
A; Cross-references: EMBL:AF001308; NID:g2104523; PIDN:AAC78706.1; PID:g2104538
A; Experimental source: cultivar Columbia
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C; Genetics:
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Sep-1999
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A;Introns: 72,3; 106/1; 136/3; 180/3; 242/3; 297/2; 323/3; 366/3; 409/2
A;Note: T10M13.16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 531;
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                                                                                                                      Pred. No. 6e-06;
                                                                                       2 REGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : : : | || || :: | | || || || || || EKIQTVIDAGVIPRLVQLLAHPSPSVLIPALRTIGNIV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLL 40
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Pred. No. 0.86;
9; Mismatches
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            50.0%; Pred. ....
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Pred. No.
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A; Status: translated from GB/EMBL/DDBJ
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35.3%;
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Best Local Similarity 36.8%;
Matches 14; Conservative
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                                           Conservative
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-538 <STO>
                  Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: pendulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
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OM protein - protein search, using sw model

July 29, 2002, 16:12:06; Search time 124.4 Seconds (without alignments) 57.016 Million cell updates/sec Run on:

US-09-641-104A-9
217
1 CSSNKPAIVEAGGMQALGLH.....TDPSQRLVQNCLWTLRNLSD Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 Total number of hits satisfying chosen parameters:

562222 seqs, 172994929 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungl:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:* sp_unclassified:* sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:* sp_phage:* sp_mhc:* 4: 7: 7: 10: 111: 12: 13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

	Description	P79321 sus scrofa	090424 brachydanio	042486 gallus gall	09d335 mus musculu	Ogn144 ciona intes	015151 homo sapien	O9bwc4 homo sapien	P70565 rattus norv	076152 ciona savid	09pvf7 brachydanio	025100 hydra magni	061229 lytechinus	018825 caenorhabdi	Ogubzl homo sapien	09v632 homo sapien	095996 homo sapien
	ΙD	P79321	3 090424	3 042486	1 090335	09NL44	015151	Q9BWC4	1 P70565	076152	3 Q9PVF7	025100	061229	018825	Q9UB21	Q9Y632	96260
	Query Match Length DB ID	117 6	780 13	781 13	781 11	769 5	745 4	745 4	745 11	773 5	729 13	806 5	821 5	811 5	733 4	1246 4	2303 4
ф	Query Match Le	100.0	100.0	100.0	97.2	89.9	85.3	85.3	85.3	85.3	83.4	79.7	72.8	35.5	33.4	33.4	33.4
	Score	217	217	217	211	195	185	185	185	185	181	173	158	77	72.5	72.5	72.5
	Result No.	ᆏ	7	ю	4	2	9	7	&	6	10	11	12	13	14	15	16

O44326 caenorhabd1	Q9z1k7 mus musculu	Q99k59 mus musculu	Q9unh3 homo sapien	Q9udw6 homo sapien	5 homo	3 ношо	Q96t31 homo sapien	3 mus	Q96t33 homo sapien	Q96t32 homo sapien	ratt	Q969q3 homo sapien	homod		O66008 moraxella c	P94931 moraxella c	Q9fn17 arabidopsis	·	Q9pw25 oreochromis	Q9slx0 oryza sativ	Q94gv3 oryza sativ	O9snc6 arabidopsis	Q9w5t9 drosophila	Q9nhp1 drosophila	Q9h614 homo sapien	Ogunq9 homo sapien	_	Q96ag6 homo sapien
5 044326		11 Q99K59	4 Q9UNH3	4 Q9UDW6	4 Q9UDW5	4 Q9BTW3	4 Q96T31	11 Q9D3K3	4 Q96T33	4 Q96T32	11 063648	4 096903	4 Q969NO	5 Q9VCL5	2 066008	2 P94931	10 Q9FN17	5 Q9N8C1		10 Q9SLX0		10 Q9SNC6	5 Q9W5T9	5 Q9NHP1	4 Q9H6L4	4 Q9UNG9	5 Q9VR04	4 Q96AG6
32.5 4 678	1.1	30.12 353	7.4	4	. 4	4.	4	4	. 4	27:4 549	4	4.	4	26.5 . 539	6.3	6.3		8.	œ		٠		. 8.5	25.8 781	5,3	25.3 259	24.9 353	4.9
17 70.5	-	19 165.5	ر غرد عار د			•	1.7	rii.	**		÷.	29 59.5	30, 4, 59.5	1	32 57	S	34 . 7 56 . 5	35 56	36.1. 56		S	39 1. 56	40 56	41 . 56	42 · · 55	43 , 55	44 : . 54	45. (54

ALIGNMENTS

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Gaps
                                                                                                                                                                                          SEQUENCE FROM N.A.
TSCHE-SMALL INVESTINE;
Winterco A.K., Fredholm M.;
Evaluation and characterization of a porcine small intestine CDNA
                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BETA CATENIN (FRAGMENT).
Sus scrofa (Pig)
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 217; DB 6; Length 117; 100.0%; Pred. No. 3e-23; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   library.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z84131; CAB06327.1; -.
HSSP; P35222; 1G3J.
Interpro; IPR00025; vārmadillo.
Pfām; PPF0514; Armadillo_seg; 2.
PROSITE; PS50176; ARM_REPEAT; 2.
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                                     117 AA
                                       PRT;
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Best Local Similarity 100.09
Matches: 41; Conservative
                                     PRELIMINARY;
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NON_TER
SEQUENCE
RESULT 1
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RESULT

B-CATENIN.

090424:

090424

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REQUENCE FROM N.A.

C. STRAIN-C-STALL/04; TISSUE-COLON;

RA ARANIN-C-STALL/04; TISSUE-COLON;

RA ARANIN-C-STALL/04; TISSUE-COLON;

RA ARANA M., Nishi K., Yoshino M., Itoh M., Ishii Y.,

RA Arawa J., Fukuda S., Fukuda S.,

A Arawa M., Nishi K., Konnoh, H., Adachi J., Fukuda S.,

A Alzawa M., Nishi K., Kayosawa H., Kondo S., Yamanaka I.,

RA Alzawa M., Nishi K., Sanon H., Kasukawa T., Saito R.,

RA Alzawa M., Matsuda H.A., Ashburner M., Balalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchi.P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi.P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schimi L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Lyons, P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

RA Sazuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Warshiami Y., Koshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Wyashiami V. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ciona intestinalis.
Eukaryota, Metazoa; Chordata, Urochordata, Ascidiacea, Phlebobranchia,
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.; "Function of a full-length mouse cDNA collection.";
                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE COLON CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 9030417H18, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:88276; Catub.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185, ARM; TSPEAT; 7.
SEQUENCE 781 AA, 85546 MW; 937538C3B5CD75D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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1. CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
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97.6%; Pred. No. 1.9e-21;
tive 0; Mismatches 1
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                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL::AK018515; BAB31250.1; -.
HSSP:.P35222; 1G3J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01'OCT-2000 (TrEMBLrel. 15, 01'OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 97.6 Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIBETA-CATENIN.
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                                                                                                                                                                                                                                                                                                                                 MEDIINE=96122902; PubMed-8562427; MEDIINE=96122902; PubMed-8562427; Kelly G.M., Erezyilmaz D.F., Moon R.T.; "Induction of a secondary embryonic axis in zebrafish occurs following the overexpression of beta-catenin."; Mech. Dev. 53:261-273(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                    Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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BDDILNE-37464068; PubMed-9322759;
Lu J., Chuong C.M., Widelitz R.B.;
"Isolation and characterization of chicken beta-catenin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Last annotation update)
                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 217; DB 13;
100.0%; Pred. No. 2.6e-22;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 217; DB 13; 100.0%; Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
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                                         780 AA
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EMBL: U82964; AAB80856.1; -.

HSSP; P35222; 1G3J.

InterPro; IPR000225; Armadillo.

Pfam; PF00514; Armadillo_seg; 12.

SMART; SW01085; ARW; 11.

PROSITE; PS56176; ARW; EPERAT; 8.

SEQUENCE 781 AA; 85438 MW; 6D20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZFIN; ZDB-GENE-980526-362; ctnnb. InterPro; IPR000225; Armadillo. Pfam; PF00514; Armadillo_seg; 12. SMARY; SM0185; ARM; 11.
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SEQUENCE 780 AA; 85542 MW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                        U41081; AAC59732.1; -. P35222; 1G3J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                         PRELIMINARY;
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Best Local Similarity
Matches 41; Conserv
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Best Local Similarity
Matches 41; Conserv
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NCBI_TaxID=9031;
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SEQUENCE

EMBL;

042486; 042486 m

RESULT 042486

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Length 781;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Umekita Y., Liao S.;
"Molecular cloning and sequencing of the rat plakoglobin cDNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                Length 745;
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                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE-PLACENTA, CHORIOCARCINOMA; Strausberg R.N. Strausberg (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sukmitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
    SMART; SM00185; ARM; 9.
PROSITE; PS50176; ARM_REPEAT; 7.
SEQUENCE 745 AA; 81744 MW; 3519A0973748BCF4 CRC64;
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34DF7BFB4748BCF4 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                            341 CPSNKPAIVEAGGMQALGKHLTSNSPRLVQNCLWTLRNLSD 381
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                                                                                                              Score 185; DB 4; L
Pred. No. 9.1e-18;
0; Mismatches 5;
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87.8%; Pred. No. 9.1e-18;
                                                                                                                                                                                                                                                                                                                                                        745 AA.
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STPAIN-SPRAGUE:DAWLEY; TISSUE-VAGINA;
                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pfam; PF00514; Armadillo_seg; 11.
SMRAT; SM00185; ARM; 12.
PROSITE; PS05176; ARM, REPEAT; 7.
SEQUENCE 745 AA; 81726 MW; 34
                                                                                                              Query Match 85.3%;
Best Local Similarity 87.8%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, JUNCTION PLAKOGLOBIN.
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EMBL; BC011865; AAH11865.1;
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TISSUE=LUNG CARCINOMA;
Strausberg R.;
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Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-8926455; PubMed-2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
Schiller D.L., Cowin P.;
"Molecular cloning and amino acid sequence of human plakoglobin, the common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989).
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                                                        Imai K., Takada N., Satoh N., Satou Y.;
Imai K., Takada N., Satoh N., Satou Y.;
"An essential role of beta-catenin in the endoderm specification of ascidian embryo.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB031543; BAA92185.1;
InterPro; IPR000225; Armadillo.
Pran; PR0014; Armadillo.seg; 11.
SWART; SM00185; ARM; 11.
SWART; SM00185; ARM; 11.
SEQUENCE 769 AA; 84703 MW; F61CC489B436E1BC CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whittock N.V., Eady R.A.J., McGrath J.A.; "Genomic Organization and amplification of the human plakoglobin
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                          Length 769;
                                                                                                                                                                                                                                                                                                                                                                      Score 195; DB 5; Length 76
Pred. No. 3.5e-19;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   745 AA.
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EMBL; AF233882; AAG16727.1; JOINED.
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MEDLINE-96157724; PubMed-8576101;
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Pfam; PF00514; Armadillo_seg; 11
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Best Local Similarity 87.8
Matches 36; Conservative
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                        NCBI_TaxID=7719;
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Cionidae;
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae;
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SEQUENCE 806 AA; 90462 MW; 689E5E982CD5051A CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Best'Local Similarity '82.9%; Pred. No. 5.2e-16;
Matches 34; Conservative 2; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugiyama T.;
"Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadillo gene family.";
Gene 172.155-159(1996).
EMBL; U36781; AAC47137.1;
HSSP; O02248; 28CT.
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MEDLINE=96257271; PubMed=8654977;
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Pfám; PF00514; Armadillo_seg; 10.
SMART; SM00185; ARM; 10.
CVÖRANIFORMES (CYPRINIGAE, Danlo.
CVÖRANIFORMES) (CYPRINIGAE, Danlo.
TYPE (1987)
                                                                                                                                               Biol: Reprod. 61:692-704(1999).
EMBL: AF099738; AADS6592.1; -.
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O61229;
O1-AUG-1998 (
O1-AUG-1998 (
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
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                                                                                                                                                                                                                                                     Score 185; DB 11; Length 745;
Pred. No. 9.1e-18;
0; Mismatches 5; Indels
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                                                               Hipakka R.A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U58858; AAB06317.1; -.
HSSP; Q02248; 2BCT.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SW00185; ARM; 8.
PROSITE; PS50176; ARM_REPEAT; 7.
SEQUENCE 745 AA; 81777 MW; 9E2F52910A7ACD41 CRC64;
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SEQUENCE 773 AA; 85217 MW; C1340CF82AFEBDAB CRC64;
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Last sequence update)
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Last annotation update)
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                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-VAGINA;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       localized maternal factor pem.";
Dev. Biol. 202:264-279(1998).
EMBL: AB012160; BAA32789:1;
HSSP; P35222; 1G3J.
Interpro; IPR002225; Armadillo.
Pfam; PF00514; Armadillo.seg; 11.
SMART; SM00185; ARM; 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL-ADHESION PROTEIN PLAKOGLOBIN.
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.8%;
Matches 36; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        076152;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.45
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=51511;
                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BETA-CATENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PVF7;
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076152

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RESULT

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RESULT 10 Q9PVF7

δ Db Q9PVF7

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Gaps

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Score 77; DB 5; Length 811; Pred. No. 0.026; 4; Mismatches 13; Indels

97D6FFDE71BDFDFF CRC64;

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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL. U46673; AAC48154.1; -.
                                                                                                                                                                                                                                                                                                                                                335 PNLVAFGGRQILANLLSHGSPRLVQSTLETLRNISD 370
                                                                                                                                                                                                                                                                                                                   . 6 PAIVEAGGMOALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                      F03880; -.
811 AA; 92227 MW;
                                                                                                                                                                                                                  Query Match
Best-Local Similarity 52.8%;
Matches: 19; Conservative
                                                                                         EMBL; , AF063646; AAC17424.1;
                                                                                                            HSSP; 002248; 3BCT.
TRANSFAC; T03880; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           648 LWNLS 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09UBZ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05Y632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09UBZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT. 14:
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                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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DR
DR
DR
SO
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X MEDLINE=94150718; PubMed=7906398;

Wilson R., Aingerson K., Baynes C., Berks M.,

Wilson R., Aingerson R., Enderson R.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

A Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,

Rarsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Randon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,

"12. Mo f contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-98104237; Pubmed=9441670;

Miller J.R., McClay D.R.;

Miller J.R., McClay D.R.;

"Changes in the pattern of adherens junction-associated beta-catenin accompany morphogenesis in the sea urchin embryo.";

Dev. Biol. 192:310-322(1997).

EMBL; U34814; ADOW.
                                                                                Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 158; DB 5; Length 821; Pred. No. 7.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR02086; Aldehyde_dehydr.
InterPro; IPR002025; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00188; ARM; 112.
PROSITE; PS00689; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
PROSITE; PS50176; ARM_REPEAT; 8.
SEQUENCE 821 AA; 89558 MW; 71E21D562A99C5AD CRC64;
                                     01-JUN-2001 (TrEMBLrel. 17, Last annotation update) BETA-CATENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 CHNNKPAIVEAGGMSALLGHLGHHSNRLVQNCLWTLRNLSD 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             811 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.8%;
78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.8°
Best Local Similarity 78.0°
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C54D1.6 PROTEIN.
C54D1.6 OR BAR-1.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=7654;
                                                                                                                                                         Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=N2;
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                                        DDT BERNAMENT BE
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Miles A., Kuipers J., Destree O., Peifer M., Clevers H.;
"Identification of APC2, a homologue of the adenomatous polyposis coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----MQALGLHLTDPSQRLVQNCLWT 35
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
van Es J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
van Es J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
Miles; A., Kuipers J., Destree O., Peifer M., Clevers H.;
"Adenômatous Polyposis Coli Homologs in Mammals and Flies.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ012652; CAB61207.1; -.
InterPro; IPR000225; Armadillo.
Pfam:; PF00514; Armadillo.
Pfam:; PF00514; Armadillo.
Pfam:; PF00514; Armadillo.
SMART; SM00185; ARM; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733. AA; .80876 MW; 09E56BE5F7032BAD CRC64;
                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72.5; DB 4; Pred. No. 0.1; 4; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01.NOV-1999 (TrEMBLrel. 12, Created)
01.NOV-1999 (TrEMBLrel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1246 AA
                                               Created)
  PRT;
                                                                                                                                                                                                                                                                                                                                         MEDLINE-99147086; PubMed=10021369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.48;
32.38;
                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Curr. Biol. 9:105-108(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.4 Best Local Similarity 32.3 Matches 21; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSSNKPAIVEAGG-----
                                                                                                                   APC2 PROTEIN (FRAGMENT).
                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         tumoun suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Y632
ID Q9
AC Q9
DT 01
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Η;
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Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E.,
Meredith D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSSNKPAIVEAGG-----35
                                                                                                                                                                        Homo sapiens (Human),
Usukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 33.4%; Score 72.5; DB 4; Length 1246; Best Local Similarity 32.3%; Pred. No. 0.19; Matches 21; Conservative 4; Mismatches 15; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "APCZ ALEGNATIVELY SPLICED CDNA Sequence.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: BINDS A 2FE-25 CLUSTER (BY SIMILARITY).
REMBU, APL10334; AAA28183.1; -.
HSSP; Q02248; 3BCT.
RINEPTO: IPR000564; 2FE-25 Eferredoxin.
RINEPTO: IPR001225; Armadillo.
RINEPTO: IPR001225; Armadillo.
RPRINTS; PR00159; 2FE-25FRDOXIN.
RPRINTS; PR00159; 2FE-25FRDOXIN.
RPRINTS; PR00159; 2FE-25FRDOXIN.
RPRINTS; PR00169; ARM: 3.
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) APC2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 LWNLS 378
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      DDT READ DR RE
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Search completed: July 29, 2002, 16:12:07 Job time: 477 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model

OM protein

July 29, 2002, 15:57:10 ; Search time 158.47 Seconds Run on:

(without alignments)
28.737 Million cell updates/sec

US-09-641-104A-6 204 1 HREGLLAIFKSGGIPALVKM.....GSPVDSVLFYAITTLHNLLL

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 segs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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122: /SIDSI/gcgdata/hold-genesegy-embl/AA1990.DAT:*
123: /SIDSI/gcgdata/hold-genesegy-embl/AA1990.DAT:*
124: /SIDSI/gcgdata/hold-genesegy-embl/AA1990.DAT:*
125: /SIDSI/gcgdata/hold-genesegy-embl/AA1990.DAT:* A_Geneseq_032802:* 99... 110... 111... 114... 114... 114... 116

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Human beta-catenin	Human beta catenin	Human beta-catenin	Novel human secret	Human beta-catenin	Mouse beta-catenin	Novel human secret	Human beta-catenin	Drosophila melanog	Drosophila melanod	Drosophila melanog
	ID		AAY33217	AAB07290	AAY70740	AAU28118	AAE06038	AAE06039	AAU28306	AAY33232	ABB60196	ABB65819	ABB65821
	DB	:	20	21	21	22	22	22	22	20	22	22	22
	Query Match Length DB		41	781	781	781	781	781	800	41	840	840	840
r	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.0	92.2	92.2	92.2
	Score		204	204	204	204	204	204	204	202	188	188	188
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ALIGNMENTS

Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor; suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth. Human beta-catenin protein armadillo repeat arm3 fragment. (DELB+) DELBRUECK CENT MOLEKULARE MEDIZIN MAX. AAY33217 standard; peptide; 41 AA. 22-FEB-1999; .99DE-1009251. 98DE-1007390 (first entry) DE19909251-A1. Homo sapiens. 21-FEB-1998; 26-AUG-1999. 18-NOV-1999 AAY33217; AAY33217 RESULT PAR NEW YORK ON THE PROPERTY OF THE PROPERTY O

J, Von Kries Birchmeier W,

WPI; 1999-470389/40.

Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor

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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides of tumor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or specific interaction domains for LEF-1, TCF-4, APC, conductin or screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin is a key compound in the Wint signalling pathway and is involved in development of tumors. Generally its interaction with LEF-1 or TCF-4 is oncogenic unit interaction with APC, conductin or E-cadherin is anti-oncogenic. (A) which inhibit interaction are particularly used to treat tumors, especially carcinoma of the colon and melanoma, but also, the cate they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth. AAY33217-Y33222 represent human beta-catenin armadillo repeat fragments described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense compounds targeting nucleic acids encoding human beta caterin (HBC) useful for treating diseases associated with HBC expression and as prophylaxis to prevent or delay infection, inflammation or tumor formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catenin; cadherin; metastasis; cadherin-associated protein; o; colorectal cancer; melanoma; antisense oligonucleotide;
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                                    Disclosure; Page 7; 16pp; German.
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Best Local Similarity 100.0
Matches 41; Conservative
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suppressor gene products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta-catenin; Wnt antagonist; contraceptive; contraceptive vaccine; oocyte development; female primate contraception; oocyte viability; monoclonal antibody; Wnt signalling.
                                 Beta, catenin is a member of the catenin family of cytosolic proteins and a key member of the Wnt signalling pathway. Catenins interact with the cytoplasmic domains of cadherin glycoproteins, and are important in maintaining cell adhesiveness. The loss of cell adhesiveness is implicated in metastrasis. Beta catenin is also known as cadherin-associated protein and is implicated in colorectal cancer and melanoma. The present sequence is the human beta catenin protein. The coding sequence of this protein was used in the present invention to design antisense oligonucleotides (AAARSIST-ASSASSG). The oligonucleotides are capable of hybridising to human beta catenin, in order, to inhibit expression of human beta catenin. The oligonucleotides may be used in gene therapy for colorectal cancer or melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contraceptive composition for inhibiting oocyte development in a female primate comprises a Wnt polypeptide antagonist
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Matches 41; Conservative
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                                                                                                                                                                                                                                                                                             781 AA;
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                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou P;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
or more armidillo-like repeats which participate in cadherin binding. Other mutants include those lacking amino acids 555-781 or 424-781, or 1-422 of beta-catenin.
                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders
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                                                                                                                  100.0%; Score 204; DB 21; Length 781; 100.0%; Pred. No. 1.7e-21; cive 0; Mismatches 0; Indels 0
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Drmanac RT, Zhang J, Chen R, Xue AJ,
                                                                                                                                                                                 Novel human secretory protein, Seq ID No 287.
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                                                                                                                                                                                                                                                                                                       AAU28118 standard; Protein; 781 AA
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2000US-0596193.
2000US-0616847.
2000US-0665363.
2000US-0693267.
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Yang Y,
                                                                                                                                  Local Similarity
                                                                 781 AA;
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17-JUN-2000;
14-JUL-2000;
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20-OCT-2000;
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Best Local S
Matches 41
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                                                                  Sequence
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Parkinson's disease, Hunchagoo's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopolesis and is useful for treating myeloid or hypphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, or ligament and/or nerve disorders, or periodontal disease. Furthermore, (I) is also useful for gut, protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems.

In addition, (I) affects blorhythms or circadian cycles of rhythms,
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                                                                                                                                                                                                                                                                                                                                                                                                   fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAUZ8020-AAUZ8395 represent novel human secreted protein amino acid sequences of the invention.
the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In: vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of beta-catenin in the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; stem cell culturing; progenitor cell; pluripotential phenotype;
transplantation; haematopoietic function; allogeneic recipient;
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ilarity 100.0%; Pred. No. 1.7e-21;
Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 41; Conserv
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Disclosure; Page 23-24; 33pp; English
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The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell in a notion of beta-catenin in a progenitor or stem cell in the outlance medium for a period sufficient for the progenitor or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells; sexpanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute containing in a host that is deficient in a particular cell lineage or inneages. The expanded cell populations are also useful in campagenate recipients. The present sequence is human beta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway intitated by Mnt proteins, which are mediators of several developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 AA;
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Gaps
                              0;
                                Indels
                                                                                 Query Match 100.0%; Score 204; DB 22; Best Local Similarity 100.0%; Pred. No. 1.7e-21; Matches 41; Conservative 0; Mismatches 0;
                                                                1 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
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Length 781;

Ā AAE06039 standard; Protein; 781 Mouse beta-catenin protein #2 (first entry) 25-SEP-2001 AAE06039; φ AAE06039

Mouse; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoletic function; allogeneic recipient; signalling pathway; beta-catenin.

Mus musculus

WO200152649-A1.

26-JUL-2001

18-JAN-2000; 2000US-0176786 17-JAN-2001; 2001WO-US01459

(STRD) UNIV LELAND STANFORD JUNIOR.

Weissman IL; Nusse R, Reya T,

WPI; 2001-465328/50. N-PSDB; AAD11165

of In vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels beta-catenin in the cell

Disclosure; Page 28-30; 33pp; English.

The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell

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in antin vitro; culture medium for a period sufficient for the progenitor oristem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in a factorial control of stem cells, e.g. to reconstitute transpandantation to restore haematopoietic function to autologous or allogeneic recipients. The present sequence is mouse beta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway initiated by whit proteins, which are mediators of several developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; parkinson's disease; burn; amyotroppic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis, bone degenerative disorder; periodontal disease; qut protection; lung; liver fibrosis; mmune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                 Gaps
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Xue AJ, Wang J;
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                                                                                                                                                                                                                                                                                              Length 781;
                                                                                                                                                                                                                                                                                                                                   Indels
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Yang Y, Drmanac RT, Zhang J, Chen R,
                                                                                                                                                                                                                                                                                                                                                                                     1 HREGLLAIFKSGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                               100.0%; Score 204; DB 22;
100.0%; Pred. No. 1.7e-21;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU28306 standard; Protein; 800 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novelthuman secretory protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               075 MAR-2000; 2000US-0519705.
19-MAY-2000; 2000US-0574454.
177-JUN-2000; 2000US-05050193.
14-JUL-2000; 2000US-0616847.
19-SEP-2000; 2000US-0665363.
20-OCT-2000; 2000US-065363.
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                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100. Matches 141; Conservative
                                                                                                                                                                                                                                                   Sequence 781 AA;
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WPI; 2001-589934/66;
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Agënts for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor
                                                                                                                                       (DELB?) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                            21-FEB-1998; 98DE-1007390.
                                                                                                                                                                       Birchmeier W, 'Von Kries J;
                                                                                                                                                                                                                                                                     suppressor gene products
                                                                                                                                                                                         WPI 1999-470389/40.
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us-09-641-104a-6.rag
                                                         4 A7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Control of the lycolated human secreted polypeptides (1) and polynucleotides (II). (I) and (II) are useful for traating inflammatory conditions such as arthritis, nephritis, Crohn's disease, inflammatory conditions such as arthritis, nephritis, Crohn's disease, inclammatory conditions such as arthritis, nephritis, Crohn's disease, and so in increasing haematopolesis, stem cell survival, bone growth conditions of the central cells are readment of one or more cancers. (II) is also useful for creating transquaic animals useful for studying modulators of the polypeptides of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral experiments of sisease, and amyotrophic lateral experiments of sisease, involved in chemotactic or chemokinetic activity, regulation of haematopolesis and is useful for treatment of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcase, for treating osteoporosis, osteoarthitis, bone degenerative culcars, or periodontal disease. Furthermore, (I) is also useful for ucers, for treating osteoporosis, osteoarthitis, bone degenerative culcars, including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasathenia gravis, allergic fungal infections, autoimmune disorders e.g. multiple sclerosis, changes in addition, (I) affects blorhythms or circadian cycles of rhythms, and conditions, such as asthma or other respiratory problems. In addition, carbellism, carbohydrate, vitamins, minerals, proviecs analgesic effects or other pain reducing effects, immune response. Aucususo-Aucususys or eliminal sequences of the invention.
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                                                                                                                                     The invention relates to novel isolated human secreted polypeptides (I)
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                                                                                                     Example 2; SEQ ID No 663; 107pp; English.
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Best Local Similarity
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which is based on substances (1) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor-suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the armadillo domain (arm units 3-8) of beta-catenin, and mutants of the specific interaction domains for LEF-1, TCF-4, APC, conductin or E-cadherin; and (c) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin is a key compound in the Wht signalling pathway and is involved in the vocogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic. (A) which inhibit interaction are particularly used to treat, tumors, especially carcinoma of the colon and melanoma, but also, where the promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth. AAY3320*Y33241 represent mutant the method of thuman, beta-catenin armadillo repeat fragments described in the method of
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                                                                          This invention describes a novel agent (A) for treating human disease
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Example 4; Fig 5; 16pp; German.
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11-JUL-2000; 2000US-0614150.
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Matches 40; Conservative
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EW; Myers

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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                                                                                                                                                                                                                                                                                  ABB65819 standard; Protein; 840
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                Ouery Match
Best Local Similarity 90.29
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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      Adams M,
                                                                                                                                  sequences (ABL01840 (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
                     2001-656860/75
                                                                                                                                                                              840 AA;
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                            N-PSDB; ABL04299
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                                                                                                                                                                                                                                                                                                                                                      pharmaceutical
                                                          interactions -
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      Venter JC,
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New isolated nucleic acid
genes from Drosophila and
interactions
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seguences (ABL01840
(ABB57737-ABB72072)
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                                                                                                                                    840 AA;
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11:JUL-2000;
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                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                             Disclosure; SEQ ID NO 7380; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 24249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 188; DB 22;
Pred. No. 4.6e-19;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.28;
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                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insectiodes, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA-sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL6176-ABL30511).
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                 Length 840;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 24255
                                                                                                                                                                                                                                                                                                                                                      229 hrqgllaifksggipalvkllsspvesvlfyaltthnill 269
                                                                                                                                                                                                                                                                                                                                 1 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                    Score 188; DB 22;
Pred. No. 4.6e-19;
                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
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                                                                                                                                                                                                                                                             92.2%;
best Local Similarity 90.2%;
Matches 37; Conservative
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2000US-0614150.
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99US-0142977
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99US-0143624
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06-AUG-1999;
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                                                                                                                                            Gaps
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0
                                                                                                        92.2%; Score 188; DB 22; Length 840; 90.2%; Pred. No. 4.6e-19; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 17655.
                                                                                                                                                                                        229 hrqg1laifksgq1palvkllsspvesvlfyaittlhn111 269
                                                                                                                                                                       1 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                        AAG16853 standard; Protein; 452 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990S-0123180
990S-0125748
990S-0125784
990S-0126264
990S-0126285
990S-0128714
990S-0128714
990S-0130077
990S-0130049
990S-0130049
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99US-0136782.
99US-0137222.
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99US-0137502.
99US-0137724.
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99US-0135629
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99US-0135124
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                                                                                                     Query Match 92.27
Best Local Similarity 90.27
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                        840 AA;
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29-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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14-MAY-1999;
14-MAY-1999;
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09-MAR-1999;
23-MAR-1999;
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1-MAY-1999;
4-MAY-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                 Arabidopsis thallana protein fragment SEQ ID NO: 57125
                        203 avieagvvprliglighsspsvlipalrtigniv 236
17. AIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLL 40
                                                                                                               AAG45495 standard, Protein; 452
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                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana.
                                                                                                                                                                          18-0CT-2000 (first
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08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
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990S-0159330
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99US-0161920.
99US-0161992.
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99US-0162142
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Best Local Similarity 35.3
Matches 12; Conservative
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09-AUG-1999;

11-AUG-1999;

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completed: July 29, 2002, 16:07:52 Search: (Job time

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 15:57:10 ; Search time 57.6 Seconds (without alignments) 17.386 Million cell updates/sec Run on:

Title: Perfect score:

US-09-641-104A-6 204 1 HREGLLAIFKSGGIPALVKM......GSPVDSVLFYAITTLHNLLL Sequence:

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231628 seqs, 24425594 residues Searched:

231628 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is deriyed by analysis of the total score distribution.

SUMMARIES

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2843 1 US-07-741-940-2 2843 1 US-08-289-548h-2 2843 1 US-08-452-654-2 2843 1 US-08-452-658B-2 2843 2 US-08-452-658B-7 2843 3 US-08-450-58B-7 2843 3 US-08-450-582-2 2843 3 US-08-450-582-2 2843 3 US-08-81-355h-7 2973 2 US-09-03-87A-7 2973 4 US-09-03-87A-7 248 1 US-09-03-87A-7 248 1 US-08-313-553-3 262 1 US-08-313-553-2 262 3 US-08-313-553-2 263 3 US-08-313-553-2 265 3 US-08-313-553-1 265 3 US-08-313-553-1 265 3 US-08-313-553-1 265 3 US-08-313-553-1	2,	2,	2,	'n	۷,	'n	7	,,	7,	7,	′,	'n	7	3,	'n	'n	15,	15,
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22 22 28 84 84 3 3 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	US-07-741-940-2	US-08-289-548A-2	US-08-452-654-2	US-08-452-655B-2	US-08-452-655B-7	US-08-370-235A-2	US-08-450-582-2	US-08-450-582-7	US-08-821-355A-7	US-09-003-687A-7	US-09-136-605-7	US-08-313-553-3	US-08-303-651-2	US-08-767-993-3	US-08-313-553-2	US-08-767-993-2	US-08-313-553-15	US-08-767-993-15
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28 29 30 31 31 32 33 34 35 36 37 38 38 39 40 40 40 40 40 40 40 40 40 40	2843	.2843	.: 2843	2843	. 2843	2843	2843	2843	. 2973	. 2973	. 2973	248	248	248	262	262	559	559
228 330 330 330 330 330 330 330 330 330 33	25.0	25,0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	24.3	24.3	24.3	24.3	24.3	24.3	24.3
9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	 . 51	51	. 51	51	51	51	. 51	(-1) 51	. : 5 51	51	51	49.5	49.5	49.5	49.5	49.5	49.5	49.5
	28	29	30	31	32.	33	34.	35	36	37	38	.68	40	41.	42	43	44	45

ALIGNMENTS

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Gaps
                                                            GENERALINFORMATION:
APFLICANT: Kosik, Kenneth S.
APFLICANT: Abid, Jiahhua
TITLE OF INVENTION: ALARW RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
STREET: 225 Franklin Street
CITY: BOSTON
STREET: 225 Franklin Street
CITY: BOSTON
STATE: MA
COUNTY: USA
COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FESTESC for Windows 95
SOFTWARE: PESTESC for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: US-08/982,785A
FILING DATE: US-08-1996
ATTORNEY/AGENT INFORMATION:
NAME: FREEDENT INFORMATION:
NAME: FREEDENT JON WINBER: 29,066
FEFTEDENT FORCKET MINBER: 29,066
FFTEDENT FORCKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05311/018001
                     Sequence 10, Application US/08982785A Patent'No. 6258929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEFERENCE/DOCKET NUMBER: 0531
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELERAX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENTH: 620 antino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.29
Best Local Similarity 40.09
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-982-785A-10
US-08-982-785A-10
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Gaps
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Sequence; 3, Application US/08982785A
Patent.No. 6258929
GENERAL: INFORMATION:
APPLICANT: Zhou, Jianhua
TITLE; OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE; OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES: 413
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                           Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 2;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPRINATING SYSTEM: Windows 95 SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Freeman, John W.
LREGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 05311/018001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               920905.90016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 GGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
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PRIOREAPPLICATION DATA:
. APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                         CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: 4 US/08/883,515
                                                                     COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               Query!Match , , 26.0%;
Best Local Similarity 46.7%;
Matches. , 14; Conservative
COMPUTER READABLE: FORM:
, MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617/542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA ..., ZIP: 02110-2804.
COMPUTER READABLE:FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-883-515-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT; '41,
US-08-982-785A-3
                                                                                                                                    · SOFTWARE:
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Pred. No. 11;
6; Mismatches 16; Indels
                                                                                                                                                         US-08-982-785A-9

Sequence 9, Application US/08982785A

Patent No. 6258929

GENERAL INFORMATION:

APPLICANT: Rosik, Kenneth S.

APPLICANT: Zhou, Jianhua

TITLE OF INVENTION: ALARM RELATED PEPTIDES AND

TITLE OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Osteryoung, Katherine W
TITLE OF INVENTION: PLANT CHLOROPLAST DIVISION GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 5
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STRATE: MA
COUNTRY: USA
COUNTRY: USA
COMPUTER: EDISKette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
COMPUTER: ISM COMPALIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
FILLING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
RECTSTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/COCKET NUMBER: 29,066
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 REGLLAIFKSGGIPALVKMLGSPVDSVLFYAIT-TLHNL 39
                           :|: |||||||||:|
196 IALKNCGGIPALVRLIRKTTDDEIRELVTGVLWNL 230
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Best Local Similarity 41.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-982-785A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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ZIP: 53701-2113
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STATE: WI
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                                                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl
APPLICANT: Corley, Neil
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN IMPORTIN ALPHA HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HUMAN IMPORTIN ALPHA HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,227
FILING DATE: Filed Herewith
152. AVVQSNAVPLFLRLLRSPHQNVCEQAVWALGNII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152' AVVQSNAVPLFLRLLHSPHQNVCEQAVWALGNII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.5%; Score 52; 29.4%; Pred. No.
                                                                                                Sequence, 3, Application US/08933227
Patent No. 5965394
GENERAL»INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence'4, Application US/08933227
Patent'No. 5965394
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 521 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl
APPLICANT: Corley, Neil
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                   3174 Porter Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELEFAX: 650-845-416b
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 29.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : GenBank
1928975
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                     STRÉET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                               94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-933-227-4
                                                                           US-08-933-227-3
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                                                                                                                                                                                                                                         Gaps
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                                                                       LOCATION: 11, 13-14, 16-18, 21, 23, 33-36, and 41-44
CTHER INFORMATION: where Xaa at positions 11, 13-14, 16-18,
CTHER INFORMATION: 21, 23, 33-36, and 41-44 is any amino acid
                                                                                                                                                                                                                                         ;;
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                                                                                                                                                                                              Score 52; DB 4; Length 44;
Pred. No. 0.54;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Guegler, Karl
APPLICANT: Corley, Neil
APPLICANT: Corley, Neil
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN IMPORTIN ALPHA HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDERSSE: CORRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,227
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY AGENT INPORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 52; DB 2;
; Pred. No. 13;
10; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLL 40
                                                                                                                                                                                                                                                                                                     1 GGIPALVRLLXNXXDXXXLLXAAXGVLRNL 30
                                                                                                                                                                                                                                                                          12 GGIPALVKMLGSPVD--SVLFYAITTLHNL 39
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08933227 Patent No. 5965394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: FELECOMMUNICATION TELECOMMUNICATION TELECOMMUNICATION TELEPHONE: 650-855-0555
                                                                                                                                                                                          25.5%;
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29.4%;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.5%
Best Local Similarity 29.4%
Matches 10; Conservative
                                                                                                                                                                                          Query Match
Best Local Similarity 46.79
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THP1PLB01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bandman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE
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; CLONE: 10403
US-08-933-227-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-08-933-227-1
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STATE:
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                                                                                                                                                                                                                                                                                                                       Length 686;
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APPLICANT: Kosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Windows 95
SOFTWARE: FREESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,785A
FILING DATE: 02-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 40.0%; Pred. No. 21;
Matches 14; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                6 LAIFKSGGIPALVKMLGSPVDSVLFYAIT-TLHNL 39
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Freeman, John W. REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET: NUMBER: 05311/018001
TELECOMMULCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
                    05311/018001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08982785A Patent No. 6258929
                                                    TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHRRACTERISTICS:
LENGTH: 686 amino acids
TYPE: amino acids
29,066
             REFERENCE/DOCKET: NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.0%;
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-982-785A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Patent No. 6258929
GENERAL INFORMATION:
APPLICANT: Kosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 2; Length 529;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZUP: 10210-2804

ZUP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKetter
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,785A
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/933,227
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATLING DATE:
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.55
Best Local Similarity 33.33
Matches 11; Conservative
                                                                                             COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
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      Palo Alto
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CITY: Boston
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    CITY: Pa
STATE: C
COUNTRY:
ZIP: 943
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COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS B VIRUS TRANSMISSION
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                                                                                                                                                                                                                                            COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51;
Pred. No.
                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155 Avenue of the Americas CITT: New York
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                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 103, Application US/08484223B Patent No. 6020459 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS F
TITLE OF INVENTION: MEMBRANE FUSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennie & Edmonds LLP
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Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)'869-9741/886.
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 103:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%;
                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 856 amino acids
TYPE: amino acid
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Best Local Similarity 33.3
Matches 15; Conservative
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                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                         New York
                                                                                                                    CITY: New York STATE: New York
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-484-223B-103
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APPLICANT:
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APPLICANT:
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     Gaps
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                                                                                                                                                                                                                   APPLICANT: Kosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 666;
24:
   Indels
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   14;
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,785A
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY AGENT INFORMATION:
                                                        Mismatches
                                  6 LAIFKSGGIPALVKMLGSPVDSVLFYAIT-TLHNL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
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Pred. No.
                                                                                                                                             US-08-982-785A-11
; Sequence 11, Application US/08982785A
; Patent No. 6258929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 103, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0531
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
 9
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Matthews, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%;
39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 666 amino acids TYPE: amino acid
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Best Local Similarity 39.4'
Matches 13; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild, Carl T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-982-785A-11
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                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                       STREET: 225 F1
CITY: Boston
STATE: MA
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14;
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APPLICANT:
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APPLICANT:
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Matches
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GENERAL'INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Compositions M.
TITLE'OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE'OF INVENTION: TRANSMISSION
TITLE'OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
COFRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 51; DB 3; Length 856;
ed. No. 33;
Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 3; Length 856;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77, HIEGLLMVFKDNIIPYSFKVRSYTKIVINILIYNGWYADSVINRH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 HREGLLAIFKSGGIPALVKMLG--SPVDSVLFY-----AITTLH 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HREGLLAIFKSGGIPALVKMLG--SPVDSVLFY-----AITTLH 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA 30,742
REFRENCE/DOCKET NUMBER: 30,742
REFRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%; Score 51; 33.3%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 103, Application US/08475668A Patent No. 6060065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     (212) 869-9741/8864
                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        25.0%;
   (212) 790-9090
                                                                                                                                                                     ENGTH: 856 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 33.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                            MOLECULE TYPE: protein
US-08-919.597-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711 ·
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Matches 15; Conserv
                                                                                                                                                                                                   amino acid
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New York
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US-08-475-668A-103
ŤELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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8
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Pred. No. 33;
6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 HTEGLLMVFKDNIIPYSFKVRSYTKIVTNILIYNGWYADSVTNRH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HREGLLAIFKSGGIPALVKMLG--SPVDSVLFY-----AITTLH 37
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLING LOLL:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY-AGENT INFORMATION:
NAME: COFUZZI, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                     APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                  7872-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 103, Application US/08919597 Patent No. 6054265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wid, Call T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 856 amino acids
TYPE: amino acids
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.0%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.0
Best Local Similarity 33.3
Matches 15; Conservative
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; MOLECULE TYPE: protein
US-08-484-2238-103
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COMPUTER READABLE FORM:
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TITLE OF INVENTION: OI
TITLE OF INVENTION: TI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1155 Av
CITY: New York
                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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us-09-641-104a-6.rai

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US-08-485-551A-103

Sequence 103, Application US/08485551A

Sequence 103, Application US/08485551A

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Matthews, Thomas J.

APPLICANT: Lambert, Dennis M.

APPLICANT: Lambert, Dennis M.

APPLICANT: Languis, Alphonse J.

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
LIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDAY
MEDIUM TYPE: FORDAY
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: O7-JUN-1995
CLASSIFICATION NUMBER: 30,742
REFERENCE/ADGORET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRANICATION NUMBER: 30,742
REGISTRATION NUMBE
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-551A-103
                                                  q
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Gaps 8; Query Match 25.0%; Score 51; DB 3; Length 856; Best Local Similarity 33.3%; Pred. No. 33; Matches 15; Conservative 6; Mismatches 16; Indels 1 HREGLLAIFKSGGIPALVKMLG--SPVDSVLFY----AITTLH 37 δλ

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QQ

Search completed: July 29, 2002, 16:05:07 Job time: 477 sec

THIS PAGE BLAMK (USPTO)

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 15:57:15 ; Search time 34.24 Seconds (without alignments) 46.364 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-641-104A-6 204 1 HREGLLAIFKSGGIPALVKM......GSPVDSVLFYAITTLHNLLL

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: 'Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P35222 homo sabien	B mus n		P26233 xenopus lae	_	P14923 homo sapien	•	_	P18824 drosophila	P35224 urechis cau		004294 arabidopsis		P38310 saccharomyc	022478 lycopersico		,	P98203 mus musculu						026973 methanobact	Q08406 rattus norv	O00505 homo sapien	_	6	_	P52292 homo sapien	P52293 mus musculu	1586	Q58194 methanococc
SUMMARIES	TI CI	CTNB HUMAN	CTNB_MOUSE	CTNB_RAT	CTNB_XENLA	PLAK_MOUSE	PLAK_HUMAN	PLAK_XENLA	ARM_MUSDO	ARM_DROME	CTNB_URECA	CTNB_TRIGR	IMA2_ARATH	VAC8_YEAST	YB57_YEAST	IMA_LYCES	ARVC_HUMAN	PKP4_HUMAN	ARVC_MOUSE	CTD1_MOUSE	CTD1_HUMAN	FTSZ_ARATH	YXXF_BACSU	EGSA_SULTO	Y887_METTH	CNTR_RAT	IMA3_HUMAN	IMA3_MOUSE	IMA4_HUMAN	IMA4_MOUSE	IMA2_HUMAN	IMA2_MOUSE	C1TC_HUMAN	HMD_METJA
	DB		Н	7	Н	Н	-	7	~	7	-	٦	-	٦	П	Н	_	٦	-	-	Н	Н	Н	П	-	Н	Н	-	1	-	-	-	-	7
	Length	781	781	781	781	7	743	738	813	843	818	820	531	578	465	527	962	1211	696	911	968	433	311	320	351	372	521	521	521	521	529	529	934	358
eF	Ouery Match	100.0	100.0	100.0	100.0	93.6	93.6	92.2	92.2	92.2	90.2	87.7	31.4	28.4	27.5	27.5	26.7	26.7		26.2		26.0								25.5				
	Score	204	204	204	204	191	191	188	188	188	184	179	64	28	26	26	54.5	54.5	54	ຕ	53.5		\sim	52.5	$^{\circ}$	25	52	52	52	52	52	52	52	51
	Result No.	· ~	7	3	4	J.	9	7	80	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33

006580 mycobacteri	014063 schizosacch	Q57689 methanococc	P03188 epstein-bar	P45128 haemophilus	P70478 rattus norv	P25054 homo sapien	Q61315 mus musculu	Q60396 apodemus sy	P09368 saccharomyc	P33073 peptostrept	P09180 drosophila	
YB28_MYCTU	IMA1_SCHPO	SYR_METJA	VGLB_EBV	MFD_HAEIN	APC_RAT	APC_HUMAN	APC_MOUSE	S124_APOSY	PUT1_YEAST	SDHA_PEPAS	RL4_DROME	
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451	. 542	999	857	1146	2842	2843	2845	.418	476	. 292	407	
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 34 . 51	35 51	36 🔆 🤥 51	37 51	38. 1., 51	39 (1 51	40-79 51	41. 151	42, 50.5	43 : .50.5	44 1: 50	45 50	٠.

ALIGNMENTS

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MOLY CELL 3:33-3-342(JUUU)

C 1-F FUNCTION INVOIVED IN THE REGULATION OF CELL ADHESION AND IN

SIGNAL TRANSDOCTION THROUGH THE WNT PATHWAY.

C 1-F SIGNAL TRANSDOCTION THROUGH THE WNT PATHWAY.

C 1-F SUBURIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION

C 1-F SUBURIT: THE CYTOSOLIC FORM BINDS TOFFLEF-1 AND MAY ALSO BIND

C 2-CADHERIN. THE NUCLEAR FORM BINDS TOFFLEF-1 AND MAY ALSO BIND

ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE

C 2-CADHERIN COMPLEX TO THE COMPLEX. TO THE NUCLEUS WHEN IT IS UNSTABLLIZED (HIGH

C 3-CADHERIN COMPLEX TO PH COMPLEX TO THE NUCLEUS WHEN IT IS

LEVEL OF PHOSPHORYLATION). TRANSLOATES TO THE NUCLEUS WHEN IT IS

LEVEL OF PHOSPHORYLATION). TRANSLOATES TO THE NUCLEUS WHEN IT IS

C 3-CATABLILIZED (LOW LEVEL OF PHOSPHORYLATION).

C 3-CATABLILIZED (LOW LEVEL OF PHOSPHORYLATION).

C 3-CATABLILIZED (LOW LEVEL OF PHOSPHORYLATION).

C 3-CATABLILIZED (LOW DITHE PROTICU IN CYTOPLASM.

C 3-CATEMIN IS REDUCED AND THE PROTICU IN CYTOPLASM.

C 3-CATEMIN IS REDUCED AND THE BETA-CATEMIN FAMILY.

C 1-SIMILARITY: CONTAINS 12 ARM REPEATS.
                               the dimerization and beta-catenin-binding region of
         .pubMed=10882138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M90364; AAA37280.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     · STANDARD;
                                                                      Cell 5:533-543(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 2BCT; 15-OCT-97.
PDB; 3BCT; 19-NOV-97.
PDB; 1DOW; 12-JUL-00.
TRANSFAC; T02984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; 3D-structure.
                          Pokutta S., Wels W.I "Structure of the di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S35091
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           MEDIINE-20337986;
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277
319
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489
                                                    alpharcatenin.
Mol. Cell 5.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535091;
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Q9WU82;
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SEQUENCE
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REPEAT
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CTNB_RAT
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AC Q9WUE
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuber A.H., Nelson W.J., Weis W.I.;
Three-dimensional structure of the armadillo repeat region of beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 118-149 IN COMPLEX WITH
                                                                                                                                                                                           PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92376536; PubMed=1509266; Butz S., Stappert J., Welssig H., Kemler R.; "Plakoglobin and beta-catenin: distinct but closely related."; Science 257:1142-1144(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 781;
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Blochem. Blophys. Res. Commun. 268:243-248(2000).
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MEDLINE-97442350; Pubmed-9298899;
Huber A.H., Nelson W.J., Weis W.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 204; DB 1;
100.0%; Pred. No. 1.3e-18;
tive 0; Mismatches 0;
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01-MAR-2002 (Rel. 41, Last annotation update)
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                     send an email to license@isb-sib.ch)
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                                                                                                                              MIM; 116606; ...
InterPro; 1PR00225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SW00185; ARM; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                  85496 MW;
                                                      EMBL; X87838; CAA61107.1; -.
                                                                   EMBL; Z19054; CAA79497.1; -. PIR; S31988; S31988. PDB; 1G3J; 17-JAN-01. TRANSFAC; T02872; -.
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Best Local Similarity 100.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Cell 90:871-882(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
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D708F170A3FBED6E CRC64;
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Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo.seg; 12.
SMART; SM00185; ARM; 11.
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224 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 264 1. HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41

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STANDARD;

CTNB_XENLA

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                                                                                                                                                                                                                                                                        -i - FUNCTION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN SIGNAL TRANSDUCTION THROUGH THE WNT PATHWAY (BY SIMILARITY).
-i - SUBUNIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND E-CADHERIN. THE NUCLEAR FORM BINDS TOF/LEF-1 AND MAY ALSO BIND PONTINS AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX TO THE CORTICAL ACTION (BY
                                                                                                                                                                           STRAIN=SPRAGUE-DAWLEY, TISSUE=Testis; MEDLINE=99428593; PubMed=10497305; Chung S.S.W., Lee W.M., Cheng C.Y.; "Study on the formation of specialized inter-Sertoli cell junctions in
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: CYTOPLASMIC WHEN IT IS UNSTABILIZED (HIGH LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS STABILIZED (LOW LEVEL OF PHOSPHORYLATION) BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED IN THE TESTIS.
-!- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED AT E30-60 DAY DPC.
-!- PTHIS FROUCED EXPRESSED IN THE TESTIS.
-!- PTM: PROBABLY PHOSPHORYLATED BY GSR-3B. WHY-DEPENDENT ACTIVATION OF DVL ANTAGONIZES THE ACTION OF GSR-3B. PHOSPHORYLATION OF BETA-CATENIN IS REDUCED AND THE PROTEIN IS NO LONGER DEGRADED,
RESULTING IN ITS ACCUMULATION IN CYTOPLASM (BY SIMILARITY).
-!- SIMILARITY: GONTAINS 12 ARM REPEATS.
                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50176; ARM REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9C29186B6DD54B87 CRC64;
             (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
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Pfam: PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
 Created)
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                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                 Beta-catenin
               16-OCT-2001
01-MAR-2002
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                                                                  CINNB1.
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                                                                                                                                                                                                                                                                  SCIENCE 224:1359-1361(1991).

-!- FUNCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL
- ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
- PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
PROPERTIES. ESSENTIAL COMPONENT OF THE VERTEBRATE WHT-SIGNALING
PATHWAY AND IS REQUIRED FOR FORMATION OF THE EMBRYONIC AXIS.
-!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                   McCrea P.D., Turck C.W., Gumbiner B.M.; "A homolog of the armadillo protein in Drosophila (plakoglobin) associated with E-cadherin.";
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Pred. No. 1.3e-18;
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                               01-MAX-1992 (Rel..22, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                            Xenopus laevis, (African clawed frog)
                                                                                                                                                                                                       MEDLINE=92073903; PubMed=1962194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARM
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              (Rel. 22, Created)
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Cell adhesion; Cytoskeleton; S
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Best Local Similarity 100.0%;
Matches: 41; Conservative 0;
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                                                                                                                             Xenopodinae; Xenopus
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                                                                                                                                           NCBI_TaxID=8355
                                                               Beta-catenin.
                                                                                                                                                                                          TISSUE-Brain;
                01-MAY-1992
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SEQUENCE
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Mismatches

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Query Match Best Local Similarity Matches 41; Conserv

Length 781; Indels

100.0%; Score 204; DB 1; 100.0%; Pred. No. 1.3e-18;

224 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 264

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93.6%; Score 191; DB 1; Length 621; 92.7%; Pred. No. 4.7e-17;
                         Indels
                         Mismatches
                          Conservative
              Best Local Similarity
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   Query Match
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Gaps

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93.6%; Score 191; DB 1; Length 743; 92.7%; Pred. No. 5.7e-17; Live 2; Mismatches 1; Indels

Conservative

Query Match Best Local Similarity Matches 38; Conserve

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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-89264555; MEDLINE-89264555; Problemed M.D., Zimbelmann R., Mueller H.M., Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M., Schiller D.L., Cowin P., "Molecular cloning and amino acid sequence of human plakoglobin, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Common junctional plaque protein,";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989).

-1-FONCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTUBAL ELEMENTS IN AN IMPORTANT
C. STRATEGIC POSITION TO INPLUENCE THE ARRANGEMENT AND FUNCTION
OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOGLOBIN IN BOTH THE DESWOSOMES AND IN THE
INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRATEGIC PROCESSION SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRATEGIC PROCESSION SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRATEGIC PROCESSION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLA -> DSSL (IN REF. 1; AAA64895).
-> A (IN REF. 1; AAA64895).
472741F400D388FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SJBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 8 ARM REPEATS.
41
                                                                                                                                                                                                                                               Oliane 1990 (Rel. 14, Last sequence update) Olimar-2002 (Rel. 41, Last annotation update) Junction plakoglobin (Desmoplakin III).
                                                                                                                                                                                                      743 AA
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ARM 5.
ARM 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000225; Armadillo.
Pfam; PF0014; Armadillo_seg; 10.
SMART; SM00185; ARM; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
                                                                                                                                                                                                                                  01.APR-1990 (Rel. 14, Created)
01.APR-1990 (Rel. 14, Last seq
01.MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50176; ARM_REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell adhesion; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;: M23410; AAA64895.1; -.
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A32905; A32905.
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139 .
743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q02248; 2BCT.
MIM; 173325; -.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                      PLAK_HUMAN
P14923;
                                                                                                                                                                                                                                                                                                    DP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                    JUP, OR
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                                                                                                                                                                         RESULT | 6 6 PLAK_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED PLAQUE PROTEIN. THE MEMBRANE-ASSOCIATED PLAQUE PROTEIN. THE MEMBRANE-ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT STRATEGIC POSITION TO INFLUENCE THE ARROGEMENT AND FUNCTION OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93093332; PubMed=1459359;
Fouquet B., Zimbelmann R., Franke W.W.;
Identification of plakoglobin in oocytes and early embryos of Xenopus laevis: maternal expression of a gene encoding a junctional Plaque protein.";
Differentiation 51:187-194(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 133-292 FROM N.A.
MEDILINE-93012479; Pubmed=1397690;
de Marais A.A., Moon R.T.;
"The armadillo homologs beta-catenin and plakoglobin are
differentially expressed during early development of Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Promise | Probest | Armeans | Promise | Prom
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-!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-!- SIMILARITY: CONTAINS 10 ARM REPEATS.
                              HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                            (Rel. 26, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                               738 AA
                                                                                                                                                                                                                                                                                                                                                      Junction plakoglobin (Desmoplakin III).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M95593; AAA49931.1; --
EMBL; X67078; CAA47463.1; --
PIR; S24636; S24636.
PIR; S35093; S35093.
HSSP; Q02248; 2BCT.
InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                       (Rel. 26, Created)
                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                01-JUL-1993
                                                                                                                                                                                                                                                                                            01-JUL-1993
01-MAR-2002
                                                                                                                                                                                                         PLAK_XENLA
P30998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laevis.
                                                                                                                                                                           PLAK_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Musca.
NCBL_TaxID=7370;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Evol. 36:224-233(1993).

- 1.5. FUNCTION: SEGMENT POLARITY PROTEIN. MUTATION IN ARM PRIMARILY
PROPECT THE POSTERIOR PART OF THE SEGMENT AND LEAD TO THE
PRODUCTION OF ANTERIOR STRUCTURES WITHIN THIS REGION. MAY BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.:
MEDILNE-93247065: PubMed-8483160;
MEDILNE-93247065: Pu
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Musca,domestica (Hōuse fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein; Segmentation polarity protein; Repeat;
Cell adhesion; Cytoskeleton; Structural protein.
DOMAIN 1 148 ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                         Length 738,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-1. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-1. SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                 ARM 9.
ARM 10.
ARM 10.
I -> V (IN REF. 2).
A -> T (IN REF. 2).
A -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                       11; HREGLLSIFKSGIPALVRMLSSPVESVLFYAITTLHNLL 251
                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                             . 11, HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                                      Score 188; DB 1;
Pred. No. 1.4e-16;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-7UL-1993 (Rel. 26, Created)
01-7UL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        813 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Armadillo segment, polarity protein.
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ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DiterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARM
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                                                                                                                                                                                                                                    ₹
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.2%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; LO4874; AAA29292:1; -.
HSSP; Q02248; IDOW
InterPro; IPR000225; Armadill
                                                                                              508 ..547.
570 ..609.
611 ..650
185 ..226
738.AA; 181711 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARM_MUSDO
                                                                                              REPEAT
REPEAT
CONFLICT
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SEQUENCE
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
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us-09-641-104a-6.rsp

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A SULPINE FERKELES.

STRAIN=ERKELES.

A Adams M. D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

A Adams M.D. Celniker S.E., Holt R.A., Band R.A., Galle R.F.,

A Adams M.D. Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

A Annantides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

A Corge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

A Britlon G.G., Wortman J.R., Yandell M.D., Champe M., Pfeiffer B.D.,

RA Barlon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Barlon R.M., Basu A., An H.-J., Andrews-Pfennkoch C., Baldwin D.,

RA Barlow R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Burtis K.C., Busam D.A., Dang Z., Mays A.D., Daw I., Dletz S.M.,

A Ghoson K. J., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G. H., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Mattei B., McIntosh T.C., McLeod M.P., Mopherson D.,
                                                                                 ÷
                                                                                                                                                                                                      Riggleman B., Wieschaus E., Schedl P., Molecular analysis of the armadillo locus: uniformly distributed transcripts and a protein with novel internal repeats are associated with a Drosophila segment polarity gene."; Genes Dev. 3:96-113(1989).
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loureiro J., Peifer M.; "Roles of Armadillo, a Drosophila catenin, during central nervous system development."; Curr. Biol. 8:622-632(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND ALTERNATIVE
                                                                                   ö
                                                           Length 813;
                                                  Score 188; DB 1; Length 81.:
Pred. No. 1.5e-16;
......rhes 1; Indels
  226 ARM 9.
567 ARM 10.
88237 MW; 73E61F59BDBFA580 CRC64;
                                                                                                                       1 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                            843 AA
                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98298928; PubMed=9635189;
                                                                                                                                                                                                                                                                                                                                                              STRAIN=OREGON-R;
MEDLINE=89211895; PubMed=2707602;
                                                              92.2%;
90.2%;
                                                                                      Conservative
                                                                                                                                                                                            STANDARD;
       626
667
      587 6
628 6
813 AA;
                                                                 Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Head;
                                                                                                                                                                                               ARM_DROME
                              SEQUENCE
        REPEAT
                    REPEAT
                                                                                                                                                                                     ARM_DROME
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REALINE-951131/4; PUDMED-722301;

REALINE-951131/4; PUDMED-722301;

READ FOLING-951131/4; PUDMED-722301;

READ FOLING-951131/4; PUDMED-722301;

READ FOLING-1 TOLGS fOr wingless signal and zeste-white 3 kinase.";

READ FOLION: NEURAL ISOFORM AND ASSOCIATE WITH CADN AND PARTICIPATE

CC -1- FUNCTION: NEURAL ISOFORM AND SIGNAL THORNATION. CAN ASSOCIATE

OF SIGNALING. ARE FUNCTION IN WG SIGNAL THANSDUCTION IS REQUIRED

SIGNALING. ARE FUNCTION OF DEFERMINATION OF NEUROBLAST FATE. ARM AND

RAD PROTEINS FUNCTION COPERATIVELY AT ADHERENS JUNCTIONS IN BOTH

ABL PROTEINS FUNCTION COPERATIVELY AT ADHERENS JUNCTIONS IN BOTH

CC -1- SIGNELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED WITH THE

CC -1- ALTERNATIVE PRODUCED SY ALTERNATIVE SPLICING.

ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC ISOFORM IS PREDOMINANT BEFORE GERM

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC ISOFORM IS PREDOMINANT BEFORE CC

CONDO IN HIGH LEVELS IN SPECIFIC CELLS ALONG THE CNS MIDLING.

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC ISOFORM IS PREDOMINANT BEFORE

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC SPECIFIC CELLS ALONG THE CNS MIDLING.

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC ISOFORM IS PREDOMINANT BEFORE

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC SPECIFIC CELLS ALONG THE CNS MIDLING.

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC ISOFORM IS PROPERRY AND FROM THE CNS MIDLING.

CC -1- TISSUE SPECIFICITY: CYTOPLASMIC SPECIFIC CELLS ALONG THE SEGMENTAL NERVES AS THEY EXIT THE CNS. BOTH ISOFORMS

INTERSEGENNTAL NERVES AS THEY EXIT THE CNS. BOTH ISOFORMS

INTERSEGENNTAL NERVES AS THEY EXIT THE CNS. BOTH ISOFORMS

CC -1- DEVELOPMENTAL STAGE: PRESENT AT ALL STAGES, BUT REACHED OF PHOSPHORYLATED ON SER, THR AND TYR RESIDUES.

C -1- TISSUE SPECIFICITY THE NUTS.

CC -1- TISSUE SPECIFICATION OF THE SECONDED OF THE CONTON OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Mount S.M., Molson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A palazpolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
As half B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
As Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A spier E., Wassarman D.A., Venter E., Wang A.H., Wang X.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A We J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Cibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
A The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-ZOLBG011; PubMed-10731137; Murphy L., Harris D., MEDLINE-ZOLBG011; PubMed-10731137; Murphy L., Harris D., Cadieu E., Barreil B.G., Ferraz C., Vidal S., Brun C., Demailber J., Borkova D., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Manana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Manana B., Kafatos F.C., Louis C., Madueno E., de Pablos B., Mapagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkiotl F., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Millian P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
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MEDLINE=95113174; PubMed=7529201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster.";
Science 287:2220-2222(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of homologues to beta-catenin/plakoglobin/armadillo in two invertebrates, Urechis caupo and Tripneustes gratilla."; Biochim. Biochi
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 818;
                                                                                                                                                                                                                                                                                                                                                                      Structural protein; Repeat.
ARM 1.
ARM 2.
ARM 3.
ARM 4.
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ARM 5.
ARM 7.
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                                                       SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 7 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 HRQGLLTIFKSGGIPALVKLLSSPVESVLFYAITTLHNLLL 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 184; DB 1;
Pred. No. 4.9e-16;
3; Mismatches 2.
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01.FEB-1994 (Rel. 28, Last sequence update)
01.MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                             InterPro; IPRO0225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMAR; SM0185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
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Σ
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REPEAT 164 203
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451
495
541
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nes 36; Conserv
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501
543
648
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                                      PROPERTIES
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P35223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in two invertebrates, Urechis caupo and Tripneustes gratilla.";
Biochim. Biophys. Acta 1173:337-341(1993).
-!- FUNCTION: BINDS TO THE CYTOPLEASMIC DOMAIN OF THE CELL-CELL.
ADHESION MOLECULE E-CADHERIN, AND PERRAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
                                                                                                                                                                                                                                                                                                                                   Developmental protein; Segmentation polarity protein; Repeat;
Cell adhesion; Cytoskeleton; Structural protein; Phosphorylation;
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Eukaryota: Metazoa; Echiura; Xenopneusta; Urechidae; Urechis
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Pred. No. 1.6e-16;
3; Mismatches 1; Indels
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ARM 11.
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ARM 12.
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
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                   send an email to license@isb-sib.ch)
                                                                      EMBL; AF001213; AAB58731.1; -.
EMBL; AE003422; AAF45688.1; ALT_INIT.
EMBL; AL021106; CAA15946.1; -.
EMBL; AL021086; CAA15946.1; JOINED.
EMBL; AL021086; CAA15935.1; -.
EMBL; AL02106; CAA15935.1; -.
                                                                                                                                                                                                                                                         InterPro; IPR000225; Armadillo.
Pfam: PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
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                                                     EMBL; X54468; CAA38350.1; -.
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HSSP; 002248; 1DOW.
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Best Local Similarity
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

MEDINE=20083488; PubMed=10617198;

MAPCINE=20083488; PubMed=10617198;

MAPCINE=20083488; PubMed=10617198;

MAPCINE=20083488; PubMed=10617198;

MAPCINE=20083488; PubMed=10617198;

MAPCINE=20083488; Marcheller C., Wambutt R.-D., Terryn N.,

MAPCINE=20083488; Marcheller C., Marcheller M., Schmidthein I.A., Reisegr M., Delseny M., Pulgdomenech P., Watson M., Schmidthein I.Y.,

RA Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidthein I.Y.,

RA Freis M., Delseny M., Pulgdomenech P., Watson M., Bourry M., Bancroft I.,

RA Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

RA Langham S.-A., McCullagh B., Billham L., Robben J.,

Nan der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

RA Langham S.-A., WcCullagh B., Billham L., Nober M., Bastiaens I., Aert R., Defoor E.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

RA Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Van den Daele H.,

RA De Keyser A., Buysshaert C., Gleben J., Villarroel R., De Clercq R.,

RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (KAP alpha).
AT4G02150 OR T10M13.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 820;
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                                                                                                                                                                                          Structural protein; Repeat.
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Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 179; DB 1; Le
Pred. No. 2.2e-15;
3; Mismatches 3;
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modified and this statement is not removed.
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Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; ILS.
PR057TE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Stru
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ilarity 85.4%;
Conservative
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489
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Salchert K.D.;
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HSSP; Q02248; 1DOW.
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RA CLERATE., Doggett 11: Hall S., Kay M., Lennard N., McLay K., Mayes R., R. Bettett A., Rajandfeam M.A., Lyne M., Benes V., Rechmann S., Bettett A., Rajandfeam M.A., Lyne M., Benes V., Rechmann S., Bettett A., Rajandfeam M.A., Grimm M., Locahnert T.-H., RA Dogs S., de Haan M., Marsea A.C., Schaefer M., Mueller-Auer B., Bargel C., Fuchs M.; Fartmann B., Grandcrath K., Dauner D., Herzl A., Rabeller R., Berger C., Monfort A., Relber R., Schmidt W., Lecharry A., Aubourg S., A., Hiller R., Schmidt W., Lecharry A., Aubourg S., R., Meber S., Herber R., Schmidt W., Lecharry A., Aubourg S., A., Phrielle B., Bent E., Johnson S., Tacon D., Jesse T., R. A., Fiben L., Schwarz S., Scholler P., Heber S., Francs P., Blelke C., R. Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Scholler P., Berneil L., Bedhia' M., Gnoj L., Schutz K., Hunng E., Spiegel L., R. Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Schodin M., Murray J., Sheet P., Cordes M., AburThreideh J., Racherille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Racherille P., Coutney L., Cloud J., Abbott A., Scott K., Johnson D., Racherille P., Coutney L., Cloud J., Abbott A., Scott K., Johnson D., Racherille P., Zhong M., Ryan E., Landrew S., Gelsel C., Layman D., Ra Dug H., All J., Berghoff A., Jones K., Drone K., Cotton M., Johnson A., Shekher M., Abricholu B., Zidandic M., Strong C., Sun H., Langra B., Zidandic M., Shekher M., Marteno A., Hameed A., Lodhi M., Johnson A., Rachen E., Marten J., Bergwa A., Hameed A., Lodhi M., Johnson A., Rachen E., Marten J., Bergwa A., Hameed A., Lodhi M., Johnson A., Rachibara M., Martenssen R., McComble W. R., Schekher M., Martenssen R., McComble W. R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHALLER 402:769-777(1999).

LITHER A SIMPLE ON BIRACTICALLY AND DIRECTLY TO SUBSTRATES CONTAINING FITHER A SIMPLE ON BIRACTICS.

EITHER A SIMPLE OR BIPARTITE NLS MOTIF. PROMOTES DOCKING OF IMPORT SIBSTRATES TO THE NUCLEAR ENVELOPE. SEEMS TO ACT AS A CYTOSOLIC SIBSTRATES TO THE NUCLEAR ENVELOPE. SEEMS TO ACT AS A CYTOSOLIC RECEPTOR FOR BOTH SIMPLE AND BIPARTITE NLS MOTIFS (BY SIMILARITY).

I. SUBUNIT: FORMS A, COMPLEX WITH IMPORTIN BETA-1 SUBUNIT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L -> P (IN REF. 2)
31AB66D246378BE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
-1: SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-1: SIMILARITY: BELONGS TO THE IMPORTIN ALPHA FAMILY
-1: SIMILARITY: CONTAINS 8 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y09511; CAA70703.1; -...
EMBL; AF001308; AAC78706.1; -...
EMBL; AL161493; CAB80708.1; -...
HSSP; Q02821; 1BK5;
Interpro; IPR000255; Armadillo.
Interpro; IPR0002652; IBB.
Fam; PF00514; Armadillo_seg; 8.
Pfam; PF001749; IBB; 1.
SMART; SM00185; ARM, ERPEAT; 4.
PROSITE; PS50176; ARM ERPEAT; 4.
Transport; Protein transport; Repeat.
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ARM 7.
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CONFLICT
SEQUENCE
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LVNAGAVPVLVSLLSSTDPDVQYXCTTALSNI 235

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| Ref Teksggiphlukmigspudsulfyaltithul 39

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                                    Gaps
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=S288C / AB972;

Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang Y.X., Catlett N.L., Weisman L.S.;
Unpublished observations (XXX-1997).
-!- FUNCTION: FUNCTIONS IN BOTH VACUOLE INHERITANCE AND PROTEIN
TARGETING FROM THE CYTOPLASM TO VACUOLE.
-!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. MOST SIMILAR TO
PLAKOGLOBINS.
                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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 DB 1; Length 531;
                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B2E75774B47E5933 CRC64;
                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
VACO OR YEL013W.
                                                                                                                                                                           578 AA.
                                                                                11; Mismatches
                                                              7 AIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLL 40
                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
31.4%; Score 64; 35.3%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .! - SIMILARITY: CONTAINS 9 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARM 1.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 6.
ARM 9.
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Pfam: PF00514; Armadillo_seg; 9.
SMART; SM00185, ARM; 8.
PR0SITE; PS50176; ARM; REPEAT; 7.
Cytoskeleton; Repeat.
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                                Conservative
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407
578 AA;
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Best Local Similarity
Matches 11; Conserv
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932
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                               12;
                                                                                                                                                                           VAC8_YEAST
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SEQUENCE
 Query Match
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                               Matches
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                                                                                                                                                                                                                                                                                       Bussereau F., Mallet L., Gaillon L., Jacquet M.;
"A 12.8 kb segment, on the right arm of chromosome II from
Saccharomyces cerevisiae including part of the DUR1,2 gene, contains
five putative new genes.";
Yeast 9:797-806(193).
-i- SÜBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.000-1998 (Rel. 36, Created)
15.000-1998 (Rel. 37; Last sequence update)
15.000-2001 (Rel. 40, Last annotation update)
1m[cort_2001 (Rel. 40, Last annotation update)
1m[cort_1n alpha subunit (Karyopherin alpha subunit) (KAP alpha).
Lycopersicon esculentum (Tomato).
Lycopersicon esculentum (Tomato).
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                01-oct-1994 (Rel. 30, Created)
01-oct-1994 (Rel. 30, itast sequence update)
16-oct-2001 (Rel. 40, itast annotation update)
Hypothetical 51.5 kDa protein in KTR3-DUR1,2 intergenic region.
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Pred. No. 7.7;
7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79EAB530D9FD0AC4 CRC64;
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                                465 AA
                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Transmembrane
                                 PRT;
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                                                                                                                                                                                                                                                                       MEDLINE=93377417; PubMed=8368014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51495 MW;
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S0000411; YBR207W.
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359
465 AA;
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Best Local Similarity
Matches 14; Conservi
                                                                                                                                  YBR207W OR YBR1446
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                              01-OCT-1994 (Rel.
                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                         STRAIN-S288C
              YB57_YEASTA
ID YB57_YEAST
AC P38310;
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14,
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ID IMA_L
AC 10247
DT 15:747
DT 15:76
DT 16:0C
DE IMPOT
OC BUKAT
OC BUKAT
OC ASPET
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Gaps

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Length 578; 15; Indels

DB 1;

Score 58; DB.1 Pred. No. 5.3; 6; Mismatches

28.4%; 34.4%;

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Conservative

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                                      Kunik T., Mizrachy L., Citcvsky V., Gafni Y.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS SPECIFICALLY AND DIRECTLY TO SUBSTRATES CONTAINING
EITHER A SIMPLE OR BIPARTITE NLS MOTIF. PROMOTES DOCKING OF IMPORT
SUBSTRATES TO THE NUCLEAR ENVELOPE. SEEMS TO ACT AS A CYTOSOLIC
RECEPTOR FOR BOTH SIMPLE AND BIPARTITE NLS MOTIFS (BY SIMILARITY).
-!- SUBUNIT: FORMS A COMPLEX WITH IMPORTIN BETA-1 SUBUNIT (BY
                                                                                                                                                         SIMILARITY).
-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-- SIMILARITY: BELONGS TO THE IMPORTIN ALPHA FAMILY.
-- SIMILARITY: CONTAINS 8 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASP/GLU-RICH (ACIDIC).
4A3F01691CEF4817 CRC64;
                                                                                                                                                                                                                                                                                                                                                               EMBL; AF017252; AAC23722.1; -.
HSSP; Q02821; 1BK5.
InterPro: IPR000225; Armadillo.
InterPro: IPR002652; IBB.
Pfam. PF00514; Armadillo_seg; 8.
Pfam; PF01749; IBB: 1.
SMART; SW00185, ARM; 8.
PROSITE; PS50176; ARM_REPEAT; 5.
Transport; Protein transport; Repeat.
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ARM 2.
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ARM 5.
ARM 6.
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                              SEQUENCE FROM N.A
NCBI_TaxID=4081;
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SEQUENCE
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150 ENTKVVIDYGSVPIFIRLLSSPSDDVREQAVWALGNI 186 3 EGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNL 39 Op õ

0

Gaps

.. 0

DB 1; Length 527;

Query Match 27.5%; Score 56; DB 1; Length 527 Best Local Similarity 29.7%; Pred. No. 8.7; Matches 11; Conservative 7; Mismatches 19; Indels

Search completed: July 29, 2002, 16:09:50 Job time: 755 sec

OM protein - protein search, using sw model

July 29, 2002, 16:04:10; Search time 124.4 Seconds (without alignments) 57:016 Million cell updates/sec Run on:

US-09-641-104A-6 204 1 HREGLLAIFKSGGIPALVKM.....GSPVDSVLFYAITTLHNLLL 41 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:*

Database :

sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_virus:* : sp_archea:*
: sp_bacteria:*
sp_fungi:*
sp_fungi:*
sp_invertebrate:*
sp_mammal:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Score Match No. Score Match 1204 100.0 2 204 100.0 3 3 194 95.1 192 93.6 6 191 93.6 6 191 100 180 88.2 111 100 78.4 113. 67 32.8 114 66 32.8 114 66 32.8				
SCORE 2014 1911 1911 1911 1911 1911 1911 1911 1	ry			
	Match Length DB	DB.	ID	Description
• •		11	Q9D335	O9d335 mus musculu
		13	042486	042486 gallus gall
		13	090424	090424 brachydanio
		Ŋ	076152	076152 ciona savid
		4	015151	015151 homo sapien
		4	O9BWC4	O9bwc4 homo sanien
		11	P70565	P70565 rattus norv
		13	Q9PVF7	Ogovf7 brachydanio
		2	O9NL44	O9n144 ciona intes
	.2 821	2	061229	061229 lytechinus
		S	Q25100	025100 hydra magni
		ß	044326	044326 caenorhabdi
		4	Q9H6L4	09h614 homo sapien
15 65 31		10	094KA9	
1		10	Q9FWY7	O9fw7 arabidopsis
16 64 31.		10	049601	

094f55 arabidopsis	Q9fht6 arabidopsis	Q9fii3 arabidopsis	Q9slx0 oryza sativ	Q94gv3 oryza sativ	Q9vrsO drosophila	Q9snc6 arabidopsis	Q9mpz5 anopheles s	Q9b293 ceratosolen	Q9b292 ceratosolen	Q9sv34 arabidopsis	Q18825 caenorhabdi	082783 oryza sativ	Q9c2k9 neurospora	Q9lzw3 arabidopsis	09fn17 arabidopsis	004286 selaginella			049602 arabidopsis	0	Q9w5t9 drosophila		Q9huh7 pseudomonas	Q96m49 homo sapien	Q9g2v2 orchesella	O88507 mus musculu	Q9sul5 arabidopsis	Q94f85 oryza sativ
					O	10 Q9SNC6	8 Q9MPZ5			10 Q9SV34		10 082783		10 Q9LZW3			10 Q94KD4			0	5 Q9W5T9		16 Q9нин7	4 Q96M49	a	11 088507		10 Q94F85
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Length 780;

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Keily-G.M., Erezyilmaz D.F., Moon R.T.;
"Induction of a secondary embryonic axis in zebrafish occurs following
"Induction of a secondary embryonic axis in zebrafish occurs following
the overexpression of beta-catenin.";
he proper secondary embryonic axis in zebrafish occurs following
meth. Job. 53.261-273(1995).
HSSP: P35222, 1033.
HSSP: P35222, 1033.
HSSP: P35222, 1033.
HSSP: P36225, Armadillo.
FRIN: ZBB-GENE-980525, Armadillo.
Frim: PRO0514: Armadillo.seg: 12.
PROSITE: PS50176; ARM. REPEAT; 8.
SEQUENCE 780.AA; 85542 MW, D7AIFB80F94066DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ciona savignyi.
Eukarýota; Metazoa; Chordata; Urochordata; Ascidlacea; Phlebobranchia;
Cionidae; Ciona.
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MEDLINE=98443204; Pubmed=9769178;

Yoshida S., Marikawa Y., Satoh N.;

"Regulation of the trunk-tail patterning in the ascidian embryo: a possible interaction of cascades between lithium/beta-catenin and localized maternal factor pem.";

Dey. Niol. 202:264-279(1998).

EMBL, AB012160; BAA32789.1;
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Eukarÿotą; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
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Pred. No. 4.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Pfam: PF00514; Armadillo_seg; 11.
SMART; SM0185; ARM; 9.
PROSITE; PS50176; ARM_REPEAT; 7.
SEQUENCE 773 AA; 85217 MW; C1340CF82AFEBDAB CRC64;
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Last annotation update)
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Pred. No. 2.4e-17;
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Best Local Similarity 87.8%; Pred. No. 4.3e
Matches 36; Conservative 5; Mismatches
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MEDLINE=96122902; PubMed=8562427;
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Best Local Similarity 95.1%;
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01,
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015151; 015093;
01-NOV-1996 (TEMBLEEL: 0
01-NOV-1996 (TEMBLEEL: 0
01-JUN-2001 (TEMBLEEL: pLAKOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=51511;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Wakaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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Isolation and characterization of chicken beta-catenin.";
Gene 196:201-207(1997).
EMBL: U82964; AAB80856.1; -.
EMBL: U82964; AAB80856.1; -.
EMBL: U82964; AAB800225; Armadillo.
Ffam; PF00514; Armadillo_Seg; 12.
FMART; SMO0185; ARM; 11.
FMART; MAROLUS ARM; 11.
FMOSITE: PS50176 ARM; 11.
SEQUENCE 781 AA; 85438 WW; 6D205D9A4DBAC562 CRC64;
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6D205D9A4DBAC562 CRC64;
                       MGD; MGI:88276; Catnb.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; PR0EPRT; 7.
SEGUENCE 781 AR, 85546 MW; 937538C3B5CD75D1 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                   100.0%; Score 204; DB 11;
100.0%; Pred. No. 1.1e-18;
tive 0; Mismatches 0;
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STRAIN-WHITE LEGHORN; TISSUE-DORSAL SKIN;
MEDLINE-97464068; Pubmed-9322759;
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                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 41; Conservative
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  HSSP; P35222; 1G3J.
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SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_FaxID=10116;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Umekita Y., Liao S.;
"Molecular cloning and sequencing of the rat plakoglobin cDNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                              Length 745;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hideaka R.A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; US8858; AAB06317.1; -.
HSSP; Q02248; 2BCT.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo.seg; 11.
SMARY; SM00185; ARM; 8.
PRĢSITE; PS50176; ARM_REPEAT; 7.
SECUENCE 745 AA; 81777 MW; 9E2F52910A7ACD41 CRC64;
                                                                                                   7.
34DF7BFB4748BCF4 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                               215 HREGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215.9REGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLL 255
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                                                                                                                                                                                                                                                          11 HREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                            Query Match , 93.6%; Score 191; DB 4; Best Local Similarity 92.7%; Pred. No. 5.7e-17; Matches 38; Conservative 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-VAGINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
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                                                     Pfam; PF00514; Armadillo_eeg; 11.
SMART; SM00185; ARM; 12.
PROSITE; PS00176; ARM_REPERT; 7
SEQUENCE 745 AA, 81726 MW; 34
                    ISSP; Q02248; 2BCT.
EMBL;; BC011865; AAH11865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FE3-1997 (TrEMBLrel. 02, 01-FE3-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19, PLAKOSLOBIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Q9PVF7 . .
ID Q9PVF7
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P70565;
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MEDLINE-90157724; PubMed=8576101;
Ozawa M., Nuruki K., Toyoyama H., Ohi Y.;
"Cloning of an alternative form of plakoglobin (gamma-catenin) lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                               Schiller D.L., Cowin P.; "Molecular cloning and amino acid sequence of human plakoglobin, the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. PubMed=11016852; Whittock N.V., Eady R.A.J., McGrath J.A.; "Genomic Organization and amplification of the human plakoglobin
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                                                                        MEDLINE-89264555; Pubmed-2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC000441; AAH00441.1; -.
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                        Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; SPEPA 7.
PROSTIE; PS50176; ARM_REPEAT; 7.
SEQUENCE 745 AA; 81744 MW; 3519A0973748BCF4 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.6%; Score 191; DB 4; L 92.7%; Pred. No. 5.7e-17; live 2; Mismatches 1;
                                                                                                                                                       common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989)
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EMBL; D50808; BAA03435.1; --
EMBL; AF306723; AA016727.1; JOINED.
EMBL; AF233882; AA016727.1; JOINED.
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TISSUE=PLACENTA, CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene.";
Exp. Dermatol. 9:323-326(2000)
                                                                                                                                                                                                                                                                                                                                                                                               the fourth armadillo repeat.";
J. Biochem. 118:836-840(1995).
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Best Local Similarity 92.7'
Matches 38; Conservative
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TISSUE=LUNG CARCINOMA;
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                                                                                                                                   MEDITINE-91104237; pubMed-9441670;
Miller J.R., McClay D.R.;
Miller J.R., hcclay D.R.;
"Changes in the patrein of adherens junction-associated beta-catenin
accompany morphogenesis in the sea urchin embryo.";
Dey. Biol. 192,310;322(1997).
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Echingidea, Buechingidea, Echinacea, Temnopleuroida, Toxopneustidae,
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Hydridae, Hydra,
NCBI_TaxID=6085;
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Best Local Similarity 73.2%; Pred. No. 8.2e-13;
Matches 30; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 821;
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Sugiyama T.;
"Identification of a Hydra homologue of the beta-
catenin/plakoglobin/armadillo gene family.";
Gene 172:155-159(1996).
EMBL: 0136781; AAC41137.1; -.
HSSP: 0002248 2BCT.
InterPro: IPR000225; Armadillo.
Pfam: PF00514; Armadillo.seg; 10.
SMART: SMO0189; ARM: 10.
SROWINE: PS50176; ARM: 10.
SROWINE: BS50176; ARM: 10.
SROWINE: BS50176; ARM: 10.
SROWINE: BS50176; ARM: 10.
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PROSIȚE; PSSO176; ARM REPEAT; 8.
SEQUENCE 821 AA; 89558 MW; 71E21D562A99C5AD CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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STRAIN=WILDTYPE 105;
MEDLINE-96257271; PubMed=8654977;
                                                                                                                                                                                                                                                                                                                                                                           PF00514; Armadillo_seg; 12.
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Matches 35, Conservative
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                                               TaxID=7654;
                                                                                                            ENCE FROM N.A.
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Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona.
NCBI_TaxID=7719;
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                                                                                            Cerda J., Reidenbach S., Pratzel S., Franke W.W.; "Cadherin-catenin complexes during zebrafish oogenesis: heterotypic junctions between complexes and follicle cells."; Biol. Reprod. 61:692_704(1999).
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
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EMBL; AB03123; BAA92185.1; -.
HSSP; P35222; 1G3J.
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ZEIN; ZDB-GENE-991207-22; Jup.
PITALE-PRO, IPRO00255; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM01085; ARW, REPEAT; 8.
PROSTITE; PS50175; ARW REPEAT; 8.
SEQUENCE 729 AA; 80033 MW; 91E00417B4FD8CEE CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-CATENIN.
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Last annotation update)
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82.9%; Pred. No. 1.3e-15;
11ve 6; Mismatches 1;
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90.2%; Score 184; DB 13;
Best Local Similarity 92.5%; Pred. No. 4.7e-16;
Matches 37; Conservative 2; Mismatches 1;
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                                            SEQUENCE FROM N.A.
MEDLINE=99386700; PubMed=10456847;
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Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; 11.
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SEQUENCE 769 AA; 84703 MW; F
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01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 82.99
Matches 34; Conservative
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                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota 'Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Makamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                             51.0%; Score 104; DB 5; Length 678; 50.0%; Pred. No. 1.9e-05; ive 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22160 FIS, CLONE HRC00266 (HYPOTHETICAL 21.9 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%; Score 67; DB 4; Length 198; 40.6%; Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AR016853; ARB94552.1; -.
EMBL; 281564; CAB04572.1; -.
HSSP; P35222; 163J.
                                                                                                                                     Costa M., Raich W., Agbunag C., Hardin J., Priess J.R., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                             E6C7ED51F6241232 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al protein.
198 Aa; 21924 MW; B637A76677FE645E CRC64;
 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        2 REGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                           198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                        InterProj IPR000225, Armadillo. Pfam. PF00514; Armadillo_seg; 6. PR051TE; PS50176; ARM_REPEAT; 1. SEQUENCE 678 AA; 74510 MW; E
 06,
06,
19,
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.09
Matches 20; Conservative
01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                         Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                              SEQUENCE FROM N.A. STRAIN=N2 BRISTOL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                       SEQUENCE FROM N.A.
                                              OR K05C4.6.
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SEQUENCE 19
                                                                                                                                                                                     Harris B.;
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; 0

Gaps

; 0

12; Indels

7; Mismatches

13; Conservative

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T14P4:3.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Vridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A..
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
Buejhler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
Howng' B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
Toriutud M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC022521; AAG10631.;
HSSP: Q02821; 18K5...
                                                                                                                                                                                                                                                                                  Capsicum annuum (Bell pepper).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bapermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                           Scylence FROM N.A..
Szurek B., Marois E., Bonas U., Van den Ackerveken G.;
Szurek B., Marois E., Bonas U., Van den Ackerveken G.;
Szurek B., Marois E., Bonas U., Van den Ackerveken G.;
Eukaryotic features of the Xanthomonas type III effector AvrBs3:
protein domains involved in transcriptional activation and the
interaction with nuclear import receptors from pepper.";
Plant J. 0:0-0(2001).
EMBL; AF369707; AAK38727.1;
SEQUENCE 529 AA; 58468 MW; FB4381AF4A889F98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 529;
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InterPro: IPR002652; IBB.
Pfam; PF00514;:Armadillo_seg; 8.
Pfam; PF01749; IBB; 1.
SMART; SM00185; ARM; 8.
PROSITE; PS50176; ARM REPEAT; 5.
SEQUENCE 538 AA; 59388 MW; 34ED12839C2EDF55 CRC64;
                                                                                                                                                                                                      01.DEC-2001 (TrEMBLrel: 19, Created)
01.DEC-2001 (TrEMBLrel. 19, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMPORRIN ALPHA 2.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE IMPORTIN ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 10; L
Pred. No. 1.7;
5; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 ENTRVVIDHGAVPIFVKLLGSPSDDVREQAVWALGNV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                            529 AA
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                          REFERENCE PALVEMENT STATEMENT SP
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Local Similarity 37.8%;
nes 14; Conservative
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Best Local Si
Matches 14;
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us-09-641-104	Gaps 0;		

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Length 538;		15; Indels
0;	1	T?
DB 10;	2.3;	ches
65;	Š.	.smat
Score 65; DB 1	Pred.	9; Mismatches
31.9%;	36.8%;	ative
	ilarity	Conserv
q	Sim	14;
Query Matc	Best Local Similarity 36.8%;	Matches

Tue Jul 30 08:15:38 2002

3 EGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNIL 40 | : : : | | | | | : : | | | | : | | : | : | | | | : | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy Dp

Search completed: July 29, 2002, 16:12:02 Job time: 472 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein July 29, 2002, 16:07:52; Search time 158.47 Seconds (without alignments) 28.737 Million cell updates/sec Run on:

US-09-641-104A-7

203 1 HQEGAMAVRLAGGLQKMVAL......NKTNVKFLAITTDCLQILAY Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 747574 segs, 111073796 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1. \(\lambda \) \(\text{SIDSI}\) \(\text{Godata}\) \(\text{Dold}\) \(\text{Godata}\) A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human beta-catenin	Human beta-catenin	Human beta catenin	Human beta-catenin	Novel human secret	Human beta-catenin	Mouse beta-catenin	Novel human secret	Drosophila melanog	Drosophila melanog	Drosophila melanog	
	D	AAY33218	AAY33233	AAB07290	AAY70740	AAU28118	AAE06038	AAE06039	AAU28306	ABB60196	ABB65819	ABB65821	
	08	20	20	21	21	22	22	22	22	22	22	22	
	Query Match Length DB ID	41	42	781	781	781	781	781	800	840	840	840	
φ	Query Match	100.0	94.8	94.8	94.8	94.8	94.8	94.8	91.9	80.5	80.5	80.5	
	Score	203	192.5	192.5	192.5	192.5	192.5	192.5	186.5	163.5	163.5	163.5	
	Result No.	1	8	3	4	Ŋ	9	7	80	6	10	11	

Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor

WPI; 1999-470389/40.

Human heta-catenin		Cosmid cHRIM5 enco	Drosophila melanog	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human protein segu	Mycobacterium spec	Drosophila melanog	Mycobacterium spec	Di-Tripeptide tran	Novel human diagno	Drosophila melanog	Human ORFX ORF2275	Chlamydia pneumoni	Drosophila melanog	Amino acid sequenc	Propionibacterium	Drosophila melanog	Human ORFX ORF1178	Novel human diagno	w	Arabidopsis thalia		Arabidopsis thalia	Sulfolobus solfata	Zea mays protein f	mays pro	ິດ	Arabidopsis thalia	Arabidopsis thalia	Zea mays protein f	Human ORFX ORF1377
AAV33217	AAY33232	AAY95707	ABB58953	AAG43632	AAG43631	AAG43630	AAB93210	AAY04792		AAY04793	AAW77727	ABG27029	ABB61302	AAB42511	AAY34593	ABB62931	AAY37015	AAU62289	ABB71470	AAB41414	ABG19122	AAR97246	AAG56231	AAG56230	AAG56229	AAW23077	AAG40686	AAG54618	AAG58401	AAG16363	AAG50044	AAG40685	AAB41613
20	202				21						19						20			21		17			21	18	21		21		7	21	21
41	41	1673	959	835	. 845	. 923	. 682	. 349	359	421	270	291	699	806	109	240	262	463	557	8	1119	. 4472	94	101	113	305	96	116	. 118	140	140	142	731
30.0	29:62	28.1	27.6	26.6	26.6	26.6	26.4	25.9	25.9	25.9	25.6	25.6	25.6	25.6	25.1	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.1	24.1	24.1		23.6	23.6	23.6	23.6		23.6	23.6
	09	. 57	56	. 54	54	54	3	52.5	52.5	$^{\circ}$. , 52	52	. 52	. 52	. 51	50	. 20	, 50	. 5.50	. 50	. 50	. 50	49	49	49	48.5	48	. 48	. 48	. 48	. 48	48	48
12	13	14	15	16	17	18	19	20	21,	22,	23.	24	25	. 92	27	. 82	59	30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; E-cabharin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ; regeneration; tissue regeneration; hair growth. Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; Human beta-catenin protein armadillo repeat arm4 fragment. (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX. Ą. AAY33218 standard; peptide; 41 98DE-1007390 99DE-1009251 Von Kries J; (first entry) Homo sapiens. Birchmeier W, DE19909251-A1 22-FEB-1999; 21-FEB-1998; 18-NOV-1999 26-AUG-1999. AAY33218; ⁻∺ ∙. AAY33218 RESULT

suppressor gene products

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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the unteraction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF+4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the armadillo domain (arm units 3-8) of beta-catenin, and mutants of the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or specific interaction domains for LEF-1, TCF-4, APC, conductin or screening substance libraries for compounds that modulate interaction of screening substance libraries for compounds that modulate interaction of the whit signalling pathway and is involved in beta-catenin to fumors. Generally its interaction with LEF-1 or TCF-4 is concogenic but interaction with APC, conductin or E-cadherin is oncogenic (A) which inhibit interaction are particularly used to treat tumors, especially caracthoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically mair growth. AAY33217-Y33222 represent human of the colon and melanoma of the colon and melanoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; wht signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth; mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 203; DB 20; Length 41; 100.0%; Pred. No. 2.6e-24; Live 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY33233 standard; peptide; 42 AA
                                   Disclosure; Page 7; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99DE-1009251.
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Best Local Similarity 100.0
Matches 41; Conservative
suppressor gene products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catenin; cadherin; metastasis; cadherin-associated protein; colorectal cancer; melanoma; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HOEGA-MAVRLAGGLOKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
94.8%; Score 192.5; DB 2
Best Local Similarity 97.6%; Pred. No. 1.2e-22;
Matches 41; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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                              Example 4; Fig 5; 16pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bennett CF, Cowsert LLM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human beta catenin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention.
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AAB07290
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WO200166689-A2.
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14 -JUL-2000; 2
19-SEP-2000; 2
20-OCT-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                              AAU28118;
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                                                                                                                           Query, Match
                                                                                                                                               Best Ľocál
Matches ′4
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                                                                                                                                                                                                                                                                                                         AAU28118
                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta-catenin; Wnt antagonist; contraceptive; contraceptive vaccine; oocyte development; female primate contraception; oocyte viability; monoclonal antibody; Wnt signalling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  administering an antegonist of a Whit polypeptide, inhibiting occyte development. Whit polypeptides are useful for promotive maturation of an immature occyte. Whit polypeptides are also useful for increasing the number of mature occytes and to enhance occyte viability. Solubbe fragments of Whit polypeptides have the ability to inhibit Whit signalling, e.g., by blocking binding of a naturally-occurring Whit protein to its receptor. They may be used to generate monoclonal antibodies which can inhibit occyte development. The present sequence is the human beta-catenin protein. Dominant negative mutants of beta-catenin lack one
                                             Beta catenin is a member of the catenin family of cytosolic proteins and a key member of the Mnt signalling pathway. Catenins interact with the cytoplasmic domains of cadherin glycoproteins, and are important in maintaining cell adhesiveness. The loss of cell adhesiveness is implicated in metastasis. Beta catenin is also known as cadherin-associated protein and is implicated in colorectal cancer and melanoma. The present sequence is the human beta catenin protein. The coding sequence of this protein was used in the present invention to design antisense oligonucleotides (AAA58327-A58566). The oligonucleotides are capable of human beta catenin. The oligonucleotides are capable of human beta catenin. The oligonucleotides may be used in gene therapy for colorectal cancer or melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patent discloses a method of female primate contraception comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contraceptive composition for inhibiting oocyte development in a female primate comprises a Wnt polypeptide antagonist
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                             21; Length 781;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      265 hqegakmavrlagglqkmvallnktnvkflaittdclqilay 306
                                                                                                                                                                                                                                                                                                                                                                                                                 1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.8e-21;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                   Query Match 94.8%; Score 192.5; Best Local Similarity 97.6%; Pred. No. 4.8 Matches 41; Conservative 0; Mismatches
           Example 13; Columns 45-52; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY70740 standard; protein; 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcmahon AP, Parr BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-317845/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta-catenin.
                                                                                                                                                                                                                                                                                      781 AA;
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                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P;
orimore armidillo-like repeats which participate in cadherin binding. Other mutants include those lacking amino acids 555-781 or 424-781, or 11422 of beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu C, Wehrman T, Ren F, Ma Y, Zhou
F, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various.human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
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                                                                                                                                                                                                                                                                      DB 21; Length 781;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        265 hqegakmavrlagglqkmvallnktnvkflaittdclqilay 306
                                                                                                                                                                                                                                                                                                                                                                                                    (1) HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                 Pred. No. 4.8e-21; ; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secretory protein, Seq ID No 287.
                                                                                                                                                                                                                                                                      94.8%; Score 192.5; 97.6%; Pred. No. 4.8
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2000US-0616847.
2000US-0665363.
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2000US-0574454
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                                                                                                                                                                                                                                                                                                                                          41; Conservative
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                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                      Sequence 781 AA;
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us-09-641-104a-7.rag

Disclosure, Page 23-24; 33pp; English.

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the polypeptide as well as for studying modulators of the polypeptides.

(1) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzhelmer's, peripheral nervous system diseases and neuropathies, such as Alzhelmer's, certivity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, culers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (1) is also useful for culers, for treating osteoporosis, osteoarthritis, bone degenerative culers, for periodontal disease. Furthermore, (1) is also useful for disorders including severe combined immunodeficiency (SCID), bacterial or reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or reperfusion, autoinmune disorders e.g. multiple sciencies and cingal infections, autoinmune disorders e.g. multiple sciencies and conditions, such as asthma or other respiratory problems. The authorities of the interval or circadian cycles of inhythms, cfertility, metabolism, catabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects immunoglobulian like care cannosition to a activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoletic function; allogeneic recipient; signalling pathway; beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 94.8%; Score 192.5; Best Local Similarity 97.6%; Pred. No. 4.8e Matches 41; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human beta-catenin protein #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD11164.
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The present invention relates to a method for in vitro expansion of mammalian stem, or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell concentration of period sufficient for the progenitor or istem cell to divide. The number of cells having the functional or stem cell to divide. The number of cells is expanded. The method is phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell pullipotential phenotype after expansion, in vitro. The expanded cell countrion in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoletic function to autobogous or alloquence recipients. The present sequence is human beta catenin protein. Beta-catenin is a pivotal player in the signalling pathway in interest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                          Score 192.5; DB 22; Length 781;
Pred. No. 4.8e-21;
0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HOEGA-MAVRLAGGLOKMVALLNKTNVKFLAITTDCLOILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 28-30; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE06039 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplantation; haematopoietic f
signalling pathway; beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse beta-catenin protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                  94.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-catenin in the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                             781 AA; ' :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-465328/50:
N-PSDB; AAD11165.
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                        t Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Example 2; SEQ ID No 663; 107pp; English.

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1;
                                                        which retain their
               or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in alogened cell populations are also useful in alogened certore haematopoietic function to autologous or allogened recipients. The present sequence is mouse beta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway initiated by Wnt proteins, which are mediators of several developmental
 an in vitro culture medium for a period sufficient for the progenitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
F, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ulcer, osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                        94.8%; Score 192.5; DB 22; Length 781; 97.6%; Pred. No. 4.8e-21; 1ve 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                      1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secretory protein, Seq ID No 663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU28306 standard; Protein; 800 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT,
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2000US-0574454.
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2000US-0665363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                             41; Conservative
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 41; Conserv
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Yang Y,
                                                                                                                                                                                                                                                       781 AA;
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19-SEP-2000;
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Zhao QA,
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Signamia Trepstrusion injury, snock, sepsis, immune responses, and is involved in increasing haematopolasis, stem cell survival, bone growth and remodeling: (1); (11) and modulators of (11) are useful for and remodeling: (1); (11) and modulators of (11) are useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (C. C. print) and responses of the polypeptides of the proliferation of neural cells and responseration of nerve and brain tissue and is useful for the treatment of central and nerves system diseases and neuropathies, such as Alzhelmer's, pertipheral nervous system diseases and neuropathies, such as Alzhelmer's, perkinson's disease, Huntington's disease, and amyotrophic lateral corparition of haematopolesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopenia and for respension of hone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, incisions, the disorders for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (1) is also useful for respension injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimment disorders e.g. multiple sclerosis, creations and conditions, such as asthma or other respiratory problems. C. In addition, (1) affects biorhythms or circadae and gravis, allergic effects or other as asthma or other respiratory problems. C. In addition, (1) affects biorhythms or circadae or elimination or alse an anique of analgasic effects or other pain reducing effects, immunoglobulin like activity and can antigen in a vaccine composition to raise an anique manner or activity and each archaen an anique manner as an anique manner and proper processed the payment of the property of the processed the payment of the processed and payment of the processed
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                                          The invention relates to novel isolated human secreted polypeptides (I) angirphyncleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischemmia-reperfusion.injury, shock, sepsis, immune responses, and is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.9%; Score 186.5; DB 22; Length 800; 95.2%; Pred. No. 4.3e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid sequences of the invention
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11-JUL-2000; 2000US-0614150.
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention isseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                   Disclosure; SEQ ID NO 7380; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 24249
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                                                                                                                                                                                                                                                                                                                                                                           Score 163.5; DB 2:
Pred. No. 1.7e-16;
3; Mismatches 4
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        Myers EW;
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          PWD,
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81.0%;
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11-JUL-2000; 2000US-0614150
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Best Local Similarity 81.0
Matches 34; Conservative
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          Adams M,
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                                      WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                     840 AA;
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                                                     N-PSDB; ABL04299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
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                                                                                                           interactions -
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           Venter JC,
                                                                                                                                                                                                                                                                                                                                      Sequence
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                              The Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, theractions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA.sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                Score 163.5; DB 22; Length 840; Pred. No. 1.7e-16; 3; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 24255; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 24255.
                                                                                                                                                                                                                                                                                                                                         270 hgdsskmavrlagglqkmvtllqrnnvkflaivtdclqilay 311
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                                                                                                                                                                                                                                                                                                                        1 HOEGA-MAVRLAGGLOKMVALLNKTNVKFLAITTDCLOILAY
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                                                                                                                                                                                                                                                          80.5%;
81.0%;
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11:JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Drosophila and
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                                                                                                            sequences (ABL01840
(ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                        Best Local Similarity
Matches (34; Conserv
                                                                                                                                                                                                           840 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB65821;
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                            Query Match
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Gaps

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Indels

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Length 840;

DB 22;

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840 AA;
Sequence
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ij Gaps 1; DB 22; Length 840; 4; Indels Score 163.5; DB 2 Pred. No. 1.7e-16; Mismatches 3; 80.5%; 81.0%; 34; Conservative Query Match Best Local Similarity Matches

1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41

δλ

270 hqdgskmavrlagglqkmvtllqrnnvkflaivtdclqilay 311 q

Ą AAY33217 standard; peptide; 41

AAY33217;

18-NOV-1999 (first entry)

Human beta-catenin protein armadillo repeat arm3 fragment.

modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; organ regeneration; tissue regeneration; hair growth

Homo sapiens

DE19909251-A1

26-AUG-1999.

99DE-1009251 22-FEB-1999;

98DE-1007390 21-FEB-1998; (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

Birchmeier W, Von Kries J;

WPI; 1999-470389/40.

Agents for treating human diseases, particularly cancer, modulate interaction of beta catenin with transcription factors or tumor suppressor gene products

Disclosure; Page 7; 16pp; German.

Example 4; Fig 5; 16pp; German.

suppressor gene products

This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides of tumor suppressor genes. The invention also describes (a) peptides (II) compressor genes. The invention also describes (a) peptides (II) trom the armadillo domain (arm units 3-8) of beta-cated molecules (III) from the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or specific interaction domains for LEF-1, TCF-4, APC, conductin or screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin development of tumors. Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is concept to the conductin or E-cadherin is concept to the conductin or E-cadherin is concept to the conduction are particularly used to the conduction are particularly to the conduction are particularly are conduction are particularly treat tumors, especially carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth. AAY33217-Y33222 represent human beta-catenin armadillo repeat fragments described in the method of the invention

41 AA; Sequence

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ij
                                                                                                                                                                                        Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; E-cadherin; screening; carcinoma; APC;
                                                                                                                                                                                                                       Wht signailing pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth; mutant.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor
                     5
y 40.0%; Score 61; DB 20; Length 41;
y 40.0%; Pred. No. 0.034;
rvative 8; Mismatches 11; Indels
                                                                                                                                                                       Human' beta-catenin protein mutant armadillo repeat arm 3.
                                                                                                                                                                                                                                                                                                                                                                  (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                        1 HQEGAMAVRLAGGLQKMVALLNK--TNVKFLAITT 33
                                                     Ä.
                                                                                                            AAY33232 standard; peptide; 41
                                                                                                                                                                                                                                                                                                                          99DE-1009251
                                                                                                                                                                                                                                                                                                                                             98DE-1007390
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                                                                                                                                                     (first entry)
                     Conservative
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           Local Similarity
nes 14; Conserv
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                                                                                                                                                                                                                                                                 Synthetic.
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    Query Match
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            Best Loca
Matches
                                                                                                    AAY33232
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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides of comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or specific interaction domains for LEF-1, TCF-4, APC, conductin or screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin is a key compound in the Wht signalling pathway and is involved in a key compound in the Wht signalling pathway and is involved in oncogenic but interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic. (A) which inhibit interaction are particularly used to treat tumors, especially carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth, AAV33230 v33241 represent mutant human beta-catenin armadillo repeat fragments described in the method of the invention

41 AA; Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of protein P14-2f encoded by an open reading frame identified in cosmid CHRIM5 (see AAA50029). CHRIM5 was obtained by ligating Xenorhabdus bovienii strain 173 (NCIMB 40986). Sau3A-digested DNA fragments into the BamH1 site of the Stratagene cosmid vector Supercos1, packaging into Escherichia coli XL Blue 1, and screening for nematocidal activity against Caenorhabdits elegans. Analysis of the DNA indicated a number of open reading frames for which the corresponding protein sequences were determined (see AAY95685-Y95735). Nematodes can be controlled through the use of bacteria associated symbiotically with an entomopathogenic nematode. Such bacteria include Xenorhabdus and Photorhabdus spp. such as X. bovienii strain 173. The symbiont bacteria, an engineered bacterium, or a nematocidal protein obtained from such bacteria. Particularly P13-1f (see AAY95706) or P14-2f can be used to control the plant protein or domesticated animal or for the control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition used to control parasitic nematodes, especially in plants such as maize, cotton, soya, and rice, comprises a bacterium which is a symbiont of an entomopathogenic nematode -
                                                  Gaps
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                                                                                                                                                                                                                                                                   Cosmid chrim5; nematocide; nematode; biological control agent; transgenic plant; helminthiasis; P14-2f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              athogen nematodes. Also claimed are vectors for nematocidal proteins in host cells, and transgenic
                        29.6%; Score 60; DB 20; Length 41; 40.0%; Pred. No. 0.048; ive 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ousley MA;
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1 hregllaifksggipalvkmlgspvdsvifyaitt 35
                                                                            1 HQEGAMAVRLAGGLQKMVALLNK--TNVKFLAITT 33
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                                                                                                                                                                                                                                              Cosmid cHRIM5 encoded protein P14-2f
                                                                                                                                                                 AAY95707 standard; Protein; 1673 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morgan JAW, Jarrett P, Ellis D,
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                                                                                                                                                                                                                    (first entry)
                                      Best Local Similarity 40.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                             Xenorhabdus bovienii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-499157/44.
N-PSDB; AAA50029.
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                            Query Match
                                                                                                                                           14
                                                                                                                                                       AAY95707
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                                                                                                     QQ
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher evexyotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 3651; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 27.6%; Score 56; DB 22; Length 959; Bestilocal Similarity 34.3%; Pred. No. 11; Matches 12; Conservative 6; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 3651.
QEGAMAVRLAGGLQKMVALLNKTNVKFLAITTDCL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers EW;
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                                                                                                                                                                            ABBŞ8953 standard; Protein; 959 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC, Adams M, Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 MAR-2001; 2001WO-US09231.
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11-JUE-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                    26-Mak-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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28.1%; Score 57; DB 21; Length 1673; 33.3%; Pred. No. 16; ive 10; Mismatches 14; Indels ;

Best Local Similarity 33.3 Matches, 13; Conservative

Query Match

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 29, 2002, 16:05:07; Search time 57.6 Seconds (without alignments) 17.386 Million cell updates/sec Run on:

US-09-641-104A-7

203 1 HQEGAMAVRLAGGLQKMVAL.....NKTNVKFLAITTDCLQILAY Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 231628 seqs, 24425594 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		æ			SUMMARIES	
Result No.	Score	Query	Query Match Length DB	ÐB	ID	Description
	52		270	4	US-08-936-165A-487	Sequence 487, App
7	20		328	7	US-08-637-759B-447	447
m	20		328	٣	US-08-871-355A-447	447
4	20	24.6	328	4	US-09-201-945-447	Sequence 447, App
ഗ	48.5	•	305	7	US-08-602-359A-42	42,
9	48		620	4	US-08-982-785A-10	10,
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80	48	Э.	756	4	US-08-982-785A-2	7
σ	47	ω,	423	4	US-08-939-366-6	9
10	47	23.2	426	9	5221737-2	
11	46	22.7	318	П	US-08-190-802A-33	m
12	46	22.7	318	4	US-08-477-346-33	33,
13	46	22.7	318	4	US-08-473-089-33	33,
14	46	22.7		٦	US-08-291-896-2	2,
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16	46	22.7		m	US-09-029-267-20	20
17	45	22.2		4	US-08-981-739-104	104
18	45	22.2		4	US-08-981-739-81	
19	45	22.2		4	US-08-931-858E-111	111
20	45	22.2	142	4	US-08-981-739-111	П
21	45	22.2		4	US-08-981-739-133	133,
22	44.5	21.9		4	US-09-094-557-3	3, Ar
23	44	21.7	791	4	US-08-861-745B-1	1,
24	44	21.7		m	US-08-463-210-9	6
25	44	21.7		4	US-09-124-900-3	Sequence 3, Appli
56	44	21.7		7	-07-743-	7
27	44	21.7	1016	7	US-07-743-357-4	4

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US-09-045-632-85	US-08-117-952-784	US-09-100-804-25	US-08-545-860D-54	PCT-US94-04496-54	5204252-6	US-08-466-886-28	US-08-469-617-28	US-08-981-739-136	US-08-836-620A-19	US-08-993-359-28	US-08-820-170A-40	US-09-055-699-40	US-09-273-565-40	US-09-565-538-40	US-09-310-187A-1	US-07-949-812-5	US-07-938-782A-2	
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28.	29.	30	31	32	33	34	32	36.3	37.0	38.	39.	40	41	42	43	44	45	

ALIGNMENTS

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APPLICANT: Hodgach, John
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Reichard, Richard
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Salthino Rosenberg, Martin
APPLICANT: Raid Housens: 534
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDEM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT CATION DATA:
CURRENT PAPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536.
                           Sequence 487, Application US/08936165A Patent No. 6348582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: GIMMI, EGWATG R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P5(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                            GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · TELEFAX: 610-270-5090
US-08-936-165A-487
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us-09-641-104a-7.rai

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COMPUTER: TELOPPY disk
COMPUTER: TELOPPY disk
COMPUTER: IBM PC COMPATIBLE
.OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
                        GENERAL: INFORMATION:
GENERAL: INFORMATION:
GENERAL: INFORMATION:
TITLE OF INFORMIN: Identification of Genes
TITLE OF INFORMINES: 501
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

24.6%; Score 50; DB

Best Local Similarity 32.4%; Pred. No. 7.3;

Matches 12; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 4 GAMAVRLAGGLOKMVALLNKTNVKFLAITTDCLOILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPMS 101 CON
                                                                                                                                   ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: RPR
TELECOMMUNICATION INFORMATION:
TELEFANCE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 447:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31,284
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION·NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             COUNTRY: USA
2IP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
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                                                                                                                                                                                                         CITY: Atlanta . STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-201-945-447
Patent No. 6015669
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                                                                                                                            DB 4; Length 270;
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                                                                                                                                                                    15; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRILING DATE: 11-DEC-1995
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: PCT/CB95/02875
FILING DATE: 13-DEC-1995
CLASSIFICATION NUMBER: PCT/CB95/02875
FILING DATE: 13-DEC-1995
CLASSIFICATION NUMBER: RPMS 101
FREGISTRATION NUMBER: RPMS 101
FREECOMMUNICATION NUMBER: RPMS 101
FREEPHONE: (404) 873-8794
INDEMATION FOR EEQ 1D NO: 447:
                                                                                                                                                                                                                                        214 ASAQAINGTLVKLIEPLGQTNYFIFLGVVAIIVTTICISILTF 256
                                                                                                                                                                                                               5 AMAVRLAGGLQKMVALLNKTN-----VKFLAITTDCLQILAY 41
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                                                                                                                                                                                                                                                                                                                                       NESOLATION OF A PROPERTY APPLICATION US/08637759B
Sequence 447, Application US/08637759B
PATENT NO. 5876910:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 7.3;
6; Mismatches
                                                                                                                       Score 52; DB .
Pred. No. 2.8;
                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-08-871-355A-447
; Sequence 447, Application US/08871355A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.68;
                                                                                                                              25.6%;
32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 amino acids
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Best Local Similarity 32.4
Matches 12; Conservative
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                                                                                                                              Query Match
Best Local Similarity 32.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                    ; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-936-165A-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ZIP: 30309-3450
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STATE: Georgia
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201 GFFAIQLPGGIYARVLLTEDNTMKFDELVQDIETLLA 237
                                                                                                                                     Sequence 447, Application US/09201945
Sequence 477, Application US/09201945
Patent No. 6442215
GENERAL-INFORMATION:
APPLICANT: David William Holden
TITLE:OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
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Gaps

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Indels

19;

DB 3; Length 328;

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Pred. No. 11;
6; Mismatches 8; Indels 1:
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Sequence 10, Application US/08982785A
Sequence 10, Application US/08982785A
GENERAL INFORMATION:
APPLICANT: Rosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.6%; Score 48; DB 4; Length 620;
45.0%; Pred. No. 32;
Live: 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                3 FGAMAVRLA-----GGLQKMVALLN--KTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Competible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSON for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,785A
FILING DATE: 02-DEC-1997
PRIOR APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET, NUMBER: 09010/010001
TELECOMMUNICATION:
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Freeman, John W.
REGISTRATION: NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 05311/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                 Query Match 23.9%;
Best Local Similarity 37.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HOEGAMAVRLAGGLOKMVAL 20
                                                                               INFORMATION FOR SEQ. ID. NO: SEQUENCE CHARACTERISTICS: EENGTH: .305 AMINO ACIDS TYPE: AMINO, ACID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO: SECUENCE CHARACTERISTICS: LENGTH: 620 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 45.0%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
COUNTY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                      MOLECTLE TYPE: PROTEIN US-08-602-359A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-982-785A-10
                                                                                                                                                                     LINEAR
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  PatentIn Release #1.0, Version #1.30
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ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; I
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/602,359A
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                  RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42, Application US/08602359A
Patent No. 5942430
GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel E.
APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIF: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         February 16, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LINK, Steven
APPLICANT: SWANSON, Ronald V.
APPLICANT: WARREN, Patrick V.
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: HAILE, LISA A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.6%;
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LINK, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 32.48
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: Februar CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-602-359A-42
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Sequence 6, Application US/08939366
Patent No. 6355415
GENERALINFORMATION:
APPLICANT: Wagner, Thomas E.
APPLICANT: Xie, Yuesheng
TITLE OF INVENTION: Compositions and Methods for the Use of
TITLE OF INVENTION: Ribozymes to Determine Gene Function
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSE: Median & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 756
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Ouery Match 23.6%; Score 48; DB 4;
Best Local Similarity 45.0%; Pred. No. 41;
Matches 9; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05311/018001
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ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
COMPUTER READABLE-FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CANADA DE LA CANADA DEL CANADA DE LA CANADA DEL CANADA DE LA CANADA DEL CANADA DE LA CANADA DEL CANADA DE LA CANADA DEL CANADA DE LA CANADA DEL CANADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | |:| |||:||:||:
541 NMENAKALRDAGGIEKLVGI 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "1, HOEGAMAVRLAGGLOKMVAL 20
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INFORMATION FOR SEQ ID-NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                756 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-982-785A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino, acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: am,
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US-08-982-785A-2
Sequence 2, Application US/08982785A
Patent No. 6258929
GENERAL INFORMATION:
APPLICANT: Rosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                             APPLICANT: KOSIK, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: MUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 686; 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,785A
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 05311/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 225 Franklin Street CITY: Boston STATE: AA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
Pred. No.
                                                                                                                                                                                                                            Sequence 8, Application US/08982785A Patent No. 6258929 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 NMENAKALRDAGGIEKLVGI 559
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Best Local Similarity 45.0'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-982-785A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Gaps
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US-08-190-802A-33
                                                                                                                                                                                                                                                                Query Match 22.7%; Score 46; DB 1; Length 318; Best Local Similarity 35.1%; Pred. No. 29; Matches 13; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.7%; Score 46; DB 4; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SECUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE: ... GBLP -CHLAMIDOMONAS HOMOLOG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     149 HIEWVSCVRFSPMTTNPIIVSGGWDKMVKVWNLTNCK 185
                                                                                                                                                                                                                                                                                                                                       ÄDDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/477,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence, 33, Application US/08477346
Patent No. 6262023
GENERAL, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 25:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 887-1500
'TELEFAX: (202) 887-0763
INPORMAŢION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MURASHIGE, KATE H
RECISTRATION NUMBER: 29
 (415) 324-0960
                                                          318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 318 amino acids
amino acid
                     FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                unknown
                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-477-346-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-477-346-33
                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: V
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                                                                                                                                                     Length 423;
                                                                                                                                                                                                                                                                                                                                                       ; Patent No. 5221737

Patent No. 5221737

Patent No. 1921737

TILLE OF INVENTION: GENE AND GENE STRUCTURE CODING FOR AN INTILE OF INVENTION: GENE STRUCTURE CODING FOR AN INCORPANSERASE, AND MICROORGANISMS WHICH EXPRESS THIS GENE NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION UNIMBER: US/07/450,230

FILING DATE: 13-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: THE FROM THE OF INVENTION: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,80?
FLLING DATE: 01-FFD-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                   DB 4;
29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 6
Pred. No. 29;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GAMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY
                                                                                                                                                                                        Mismatches
                                                                                                                                                   Score 47;
                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...med DATE: US/08/190,802A CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY ACENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 84.875
REERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dehlinger & Associates STREET: P.O. Box 60850 CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/08190802A Patent No. 5519003 GENERAL INFORMATION:
                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                 169 GGIQKMISSQSFPETQFIAVT 189
                                                                                                                                                                                                                           12 GGLQKMVALLNKTNVKFLAIT 32
                                                                                                                                                 23.2%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.2%;
Best Local Similarity 36.8%;
Matches 14; Conservative
               423 amino acids
                                                                                                                             Query Match
Best Local Similarity 38.1v
Best Local 8; Conservative
SEQUENCE CHARACTERISTICS
                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-933-366-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 426
5221737-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-190-802A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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us-09-641-104a-7.rai
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APPLICANT: Legoux, Richard
APPLICANT: Legoux, Philippe
APPLICANT: Lelong, Philippe
APPLICANT: Lelong, Philippe
APPLICANT: Salome, Marc Louis Victor
APPLICANT: Salome for fragmenting N-acetylheparos
NUMMER OF SEQUENCES:
ACCRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
ADDRESSEE: Accobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 820;
                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
.SOFTWARE: PC-DOS/MS-DOS
.SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
.APPLICATION NUMBER: US/08/291,896
.TIGNED DATE: 17-AUG-1994
.CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 1
Pred. No. 94;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: "C-LOSAMS-DOS SOFTWARE: Patentin Release #1.0, Ver. GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,278
FTLING DATE: 07-UN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: FR 93/10050
FILING DATE: 17-MG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/291,896
FILING DATE: 17-MG-1994
ATTORNEY/AGENT: INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REGISTRATION NUMBER: P58114NA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594 EGDVSLAVGGGISSQLKLFNSDNTK 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EGAMAVRLAGGLQKMVALLNKTNVK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08485278 ; Patent No. 5820857
                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS /MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.7%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 820 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 393-5350 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     LENGTH: 820 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: Z0004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                        single
                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query, Match
Best Local Similarity.
Matches 8; Conserva
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-485:278-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA fragment carrying the gene encoding the enzyme for fragmenting N-acetylheparosan and the adjacent sequences permitting its expression, recombinant enzyme intended for fragmenting N-acetylheparosan and its use.
                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; INDIVIDUAL ISOLATE: GBLP -CHLAMIDOMONAS HOMOLOG, Fig. 16 US-08-473-089-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.7%; Score 46; DB 4; Length 318; 35.1%; Pred. No. 29;
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STREET: 2000 Pennsylvania Avenue, NW
COUNTY: USA
ZIP: 20006-1812
COMPUTER: Eloppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CLASSIFICATION DATA:
APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                   Indels
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                                                                                                                149 HTEWVSCVRFSPMTTNPIIVSGGWDKMVKVWNLTNCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HQEGAMAVR-----LAGGLQKMVALLNKTNVK 27
                                                                                    1 HQEGAMAVR -----LAGGLQKMVALLNKTNVK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPAS (202) 887-0763
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
               Pred. No. 29;
                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08291896 Patent No. 5480800 GENERAL INFORMATION:
                                                                                                                                                                                                                                                       Sequence 33, Application US/08473089
Patent No. 6342368
               35.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.79
Best Local Similarity 35.19
Matches 13; Conservative
                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
            Best Local Similarity
Matches 13; Conserv
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US-08-291-896-2
                                                                                                                                                                                                                                       US-08-473-089-33
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-278-2
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0; Gaps Query Match
22.7%; Score 46; DB 2; Length 820;
Best Local Similarity 32.0%; Pred. No. 94;
Matches 8; Conservative 6; Mismatches 11; Indels

ő

3 EGAMAVRLAGGLQKMVALLNKTNVK 27 || ::: :| : | | | | | 594 EGDVSLAVGGISSQLKLFNSDNTK 618 δ

Ω

Search completed: July 29, 2002, 16:05:08 Job time: 478 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

 protein search, using sw model OM protein

Run on:

July 29, 2002, 16:09:10 ; Search time 70.63 Seconds

(without alignments)
55.779 Million cell updates/sec

US-09-641-104A-7 203 1 HQEGAMAVRLAGGLQKMVAL......NKTNVKFLAITTDCLQILAY Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

70	Description	beta-catenin - Afr	1	•		hypothetical prote		plakoglobin - mous	plakoglobin - Afri		plakoglobin, desmo	NADH dehydrogenase	AcOrf-120 protein	ACMNPV orf120 - Bo	two-component hybr	50S ribosomal prot	probable acyl-CoA	hypothetical prote			0	hypothetical prote	NADH dehydrogenase	NADH dehydrogenase	hypothetical prote	hypothetical prote			-eaı	probable glucose-6
SUMMARIES	ΙD	535099	A38973	S35091	S33794	533793	T12689	S35092	S35093	JC4835	A32905	T11032	A72865	T41857	AH2264	G81146	C83278	T01511	G70728	C81875	B86395	T06606	T11203	T11334	T00440	C96831	A96834	н87290	EDBE11	C71546
	DB	5	~	7	ď	7	7	7	7	7	7	7	7	7	7	~	~	~	~	7	7	7	~	7	7	~	7	7	~	7
	Length	781	781	781	820	817	843	621	738	908	744	607	82	82	407	190	379	571	349	190				909	526	920	370	399	775	256
•	Query Match	94.8	94.8	94.8	84.0	82.5	80.5	79.6	9.62	75.6	62.1	27.3	26.4	26.4	26.4	26.1	26.1	26.1	25.9	25.6	25.4	25.4	25.4	25.4	25.1	25.1	24.9	24.9	24.9	24.6
	Score	192.5	192.5	192.5	170.5	167.5	163.5	161.5	161.5	153.5	126	55.5	53.5	53.5	53.5	53	53	53	52.5	52	51.5	51.5	51.5	51.5	51	51	50.5	50.5	50.5	20
	Result No.	1	8	m	4	2	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

10 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	conserved hypothet	probable type III	hypothetical prote	hypothetical prote	hypothetical prote	erythrocyte membra	acetyltransferase	3-methyl-2-oxobuta	protein H06H21.10	phosphoribosyl-AMP	hypothetical prote	hypothetical prote	hypothetical prote	NADH dehydrogenase	NADH dehydrogenase	NADH dehydrogenase
50 24 6 50 24 6 50 24 6 50 24 6 50 24 6 49 50 24 6 49 50 24 1 49 2 23 9 48 5 23 9 48 5 23 9	F90016	AB0697	875900	B98265	T49992	A39707	T44838	AD1996	A88679	SHNC	T02206	T18825	T48984	C90619	T11529	C90613
50 24 6 50 24 6 50 24 6 50 24 6 50 24 6 49 50 24 6 49 50 24 1 49 2 23 9 48 5 23 9 48 5 23 9	7	7	7	7	7	7	7	7	7	Н	~	7	7	7	7	7
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	 10 50	11 50	12 , 50	13 , 50	14 50	15 15 49.5	16 . 49	- 7	18 : 49	67 61	67 : .: 01	11 48.5	12 : 48.5	13 48.5	14 . 48.5	15 : - 48.5

ALIGNMENTS

7

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Deta-catenin - African clawed frog
C;Species: Xenopus laevis.(African clawed frog)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S35099.
R;McCrea; P.D.; Turck, C.W.; Gumbiner, B.
Science 254, 1359-1361, 1991
A;Title: A homolog of the armadillo protein in Drosophila (plakoglobin) associated with A;Reference number: S35099; MUID:92073903
                                                                                                                                                                                                                                                                                                                            A; Accession: S35099
A; Molecule type: mRNA
A; Residues: 1-781 < MCC>
A; Residues: 1-781 < MCC>
A; Cross-references: GB: M77013; NID: 9214020; PIDN: AAA49670.1; PID: 9214021
C; Keywords: cytoskeleton
```

Gaps ij Length 781; Indels Score 192.5; DB 2; Pred. No. 4.1e-18; 0; Mismatches 0; Query Match 94.8%; Best Local Similarity 97.6%; Matches 41; Conservative

1;

1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41 a ŏ

265 HQEGAKMAVRLAGGLQKWVALLNKTNVKFLAITTDCLQILAY 306

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 26:Jan-1996 #sequence_revision 08-Feb-1996 #text_change 08-Oct-1999
C; Date: 26:Jan-1996 #sequence_revision 08-Feb-1996 #text_change 08-Oct-1999
C; Accession: A38973; S55356; S31988
R; Huelsken, J; Birchmeier, W.; Behrens, J.
Cell. Biol. 127, 2061-2069, 1994
A; Title: E-cadherin and APC compete for the interaction with beta-catenin and the cyt
A; Reference number: A38973; MulD:95105247
A; Reference number: a38973; MulD:95105247
A; Status: nucleic acid sequence not shown
A; Molecule.type: mRNA
A; Residues: 1-781 <HUE>
A; Residues: 1-781 <HUE>
A; Cross: references: GB: 19054; NID:938519; PIDN:CAA79497.1; PID:938520
A; Experimental source: placenta
R; Nollet, F; Berx, G; Molemans, F; van Roy, F.
Submitted to the EMBL Data.Library, June 1995
A; Description: H. sapiens beta-catenin mRNA.
A; Reference number: S53356
A; Accession: S53556
A; Accession: S53556

A; Status: preliminary

A; Molecule, type: mRNÅ A; Residués: 1-781 <001. A; Cross-references: EMBL: 87838; NID:91154853; PIDN:CAA61107.1; PID:9860988 C; Comment: The cytoplasmic protein beta-catenin normally binds to a region in the cyt

- 300 - 45 - 101

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g ò

RESULT 3 S35091 beta-catenin - mouse

0

ch 94.8%; Score 192.5; DB 2 1 Similarity 97.6%; Pred. No. 4.1e-18; 41; Conservative 0; Mismatches 0

Query Match Best Local Similarity Matches 41; Conserv

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Genes Dev. 3, 96-113, 1989
A, Title: Molecular analysis of the Armadillo locus: uniformly distributed transcripts
A, Reference number: A31861; MUID:89211895
hypothefical protein - spoonworm (Urechis caupo)
C; Species furechis caupo
C; Date fligh Mar-1997 #text_change 01-Aug-1997
C; Date fligh Mar-1997 #seguence_revision 19-Mar-1997 #text_change 01-Aug-1997
C; Date fligh Mar-1997 #seguence_revision 1997
Biochim flight Mar-1997 #seguence_revision 1997
A; Title flight Mar-1997 #seguence_revision 1997
A; Reference number: 533793; MuID: 93305730
A; Reference number: 533793; MuID: 93305730
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A; Residues: 1-843 < FBRS
A; Residues: 1-843 < FBRS
A; Crossive ferences: EMBL: AL021106; NID:e1371406; PID:e1249776; PIDN:CAA15946.1
A; Experimental source: Clone cosmid 63812
A; Experimental source: Clone cosmid 63812
B; Riggleman, B.; Wieschaus, E.; Schedl, P.
Genes Dey. 3, 96-113, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      armadillo segment polarity protein - fruit fly (Drosophila melanogaster)
Nalletrate names: protein 8684.6
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Date: 13.7409-1999 # sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C.Accession: T12689; A31861.
R.Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
R.Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
A.; Description: Sequencing the distal x chromosome of Drosophila melanogaster.
A.; Reference number: Z17572,
A.; Accession: T12689
A.; Status: Preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plakoglobin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S;5092
R;Butz, S; Stappert, J; Weissig, H; Kemler, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A; Molecule, type: DNA
A; Residues: 1-843 <RIG>
A; Cross-references: EMBL:X54468; NID:g7610; PIDN:CAA38350.1; PID:g7611
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 817;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 HQEGSKMAVRLAGGLQKMVLLLQRNNLKFLAITTDCLQILAY 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 167.5; DB 2;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HOBGA-WAVRLAGGLOKMVALLNKTNVKFLAITTDCLOILAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. HOEGA-MAVRLAGGLOKMVALLNKTNVKFLAITTDCLQILAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: FlyBase:FBgn0000117
A;Introns: 11/1; 557/3; 624/3; 715/3; 748/1
A;Note: 96E4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity, 81.0%;
Matches: , 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Watch
Best Local Similarity 83.3%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                         A Status: preliminary
A Molecule type: mRNA
A, Residues: 1-817 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT. 7
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Biochim. Biophys. Acta 1173, 337-341, 1993
A;Itile: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver
A;Reference number: S33793; MUID:93305730
A;Accession: S33794
                                                                poly
                                                                   adenomatous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C; Accession: S35091
R; Butz, S.: Stappert, J.; Weissig, H.; Kemler, R.
Science 257, 1142-1144, 1992
A; Title: Plakoglobin and beta-catenin: distinct but closely related.
A; Reference number: S35091; MUID:92376536
A; Accession: S35091
A; Accession: S35091
A; Status: preliminary
A; Molecule type: manA
A; Residues: 1-781 < BUTS
A; Residues: 1-781 < BUTS
C; Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein - sea urchin (Tripneustes gratilla)
C;Species: Tripneustes gratilla
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C;Accession: S33794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 781;
                                                                      beta-catenin are regulated in part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                               microfilament network.
C;Comment: Cellular levels of beta-catenin are regulated in particological growth.
G;Genetics:
A;Genetics:
A;Gene: GDB:CTNNB1; CTNNB
A;Cross-references: GDB:141922; OMIM:116806
A;Gross-references: GDB:141922; OMIM:116806
C;Keywords: apoptosis; carcinogenesis; cell adhesion; cytosol E;R:151-676/Region: 40-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Op õ

Score 192.5; DB 2; Pred. No. 4.1e-18; 0; Mismatches 0;

94.8%; nilarity 97.6%; Conservative 0

Best Local Similarity Matches 41; Conserv

Query Match

281

ò g

DB 2;

Score 170.5; DB 2;
Pred. No. 4.3e-15;
3; Mismatches 2;

84.0%; 85.7%;

Conservative

Query Match Best Local Similarity Matches 36; Conserv

A; Accession: \$33794 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-820 <ROS>

ä

Gaps

ij

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plakoglobin, desmosomal. - human
C;Species: Homo sapiens (man)
C;Date: 22.Nov-1989 #seguence_revision 22-Nov-1989 #text_change 29-Aug-1997
C;Accession: A32905
R;Franks, W.W.; Goldschmidt, M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cow
Proc. Natl. Acad. Sci. U.S.A. 86, 4027-4031, 1989
A;Title: Molecular cloning and amino acid sequence of human plakoglobin, the common j
A;Reference number: A32905; MUID:89264555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross.references: EMBL:AF090337; NID:94887659; PID:94887670; PIDN:AAD32262.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - redhead mitochondrion C;Species: mitochondrion Aythya americana (redhead) C:Date::16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 07-Dec-1999 C;Accession: T11032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.M.C.S.S.C.O. 1110.2. Sorenson, M.D.; Dimcheff, D.E. Proc. Natl. Acad. Sci. U.S.A. 95, 10699-10697, 1998
A.Title: Multiple independent origins of mitochondrial gene order in birds. A; Reference number: 217242
A; Reference number: 217242
A; Accession: T11032
A; Actual: preliminary; translated from GB/EMBL/DDBJ
A; Releating: DNA
A; Residues: 1-607 <JOH>
                                                                  Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 607;
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                                                                                                                                  Indels
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                                                                                                                                                                          256 YQEGAKMACAGRRAQKMVPLLNKNNPKFLAITTDCLQLLLAY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                      DB 2;
                                                                  Score 153.5; DB 2;
Pred. No. 8.8e-13;
2; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 126; DB 2;
Pred. No. 4.6e-09;
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                                                                                                                               5;
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                                                               Query; Match . 75.6%;
Best Local Similarity 81.0%;
Matches , 34; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross.references: GDB:126565;
A;Map position: 7pter-7qter
C;Keywords; cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 65.99
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 27.39
Best Local Similarity 40.09
Matches 14; Conservative
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A,Molecule:type: mRNA
Residues: 1-744 <FRA>
A,Cross-references: GB.M23410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A32905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plakeglobin - African clawed frog
CiSpecies: Xenopus laevis (African clawed frog)
CiSpecies: Xenopus laevis (African clawed frog)
CiSpecies: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
CiAccession: 835033, 824636
CiAccession: 835033, 824636
CiAccession: 535033, Mulb: 9309332
Airlie: Identification of plakeglobin in cocytes and early embryos of Xenopus laevis: Airlie: Identification of plakeglobin in cocytes and early embryos of Xenopus laevis: Airlie: preliminary
Airlie: preliminary
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A; Title: Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadillo
A; Reference number: JC4835; MUID:96257271
A; Accession: JC4835
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-806 <HOB>
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C;Comment: This protein plays roles in cadherin-mediated cell adhesion and in signal
C;Genetics:
A;Gene: betaCtn
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R; Hobmayer, B.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Hydra magnipapillata
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                       A,Title: Plakoglobin and beta-catenin: distinct but closely related. A,Reference number: S35091; MUID:92376536
A,Accession: S35092
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1.621 - GBUT>
A,Cross-references: EMBL:M90365
C,Keywords: cytoskeleton
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                                                                                                                                                                                                                                                                                                                                                     Length 621;
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A;Molecule type: mRNA
A;Roaldues: 133-184,'V',186-225,'T',227-292 <DEM>
A;Residues: 133-184,'V',186-225,'T',227-292 <DEM>
C;Coss-references: EMBL:X67078; NID:965252; PID:965253
C;Keywords: cytoskeleton
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                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY
                                                                                                                                                                                                                                                                                                                                                 Score 161.5; DB 2
Pred. No. 5.4e-14;
2; Mismatches 4
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A;Reference number: S24636
A;Accession: S24636
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83.3%;
                                                                                                                                                                                                                                                                                                                                              Query Match 79.6%;
Best Local Similarity 83.3%;
Matches 35; Conservative 3
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Science 257, 1142-1144, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 35; Conserv
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Score 53.5; DB 2; Pred. No. 19; 7; Mismatches 13;

17;

Length 407;

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RESULT 15
GB1146

GB1146

GS ribosomal protein L25 NWB0876 [imported] - Neisseria meningitidis (strain MC58 se 50s ribosomal protein L25 NWB0876 [imported] - Neisseria meningitidis
C:Dete..31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: GB1146.
R:Tettelin, H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Hickey, E.K.; 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoll, R.; A;Atchers connaber: A81000; MUID:20178755
A;Reference number: A81000; MUID:20178755
A;Stellininary
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A;Molecüle: type: DNA
A;Residües: 1-407 <KUR>
A;Cross_teferences: GB:BA000019; PIDN:BAB75370.1; PID:g17132804; GSPDB:GN00179
A;Cross_teferences: GB:BA000019; PIDN:BAB75370.1; PID:g17132804; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alb3671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: July 29, 2002, 16:09:11
                                                                                                                                                                                                                                                                                                                                                                                26.4%;
Local Similarity 22.5%;
les 9; Conservative 17
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Job time: 721 sec
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DAR Res. 8, 205-213, 201
A.Tritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A.Reference number: AB1807; MUID:21595285; PMID:11759840
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J. Gen. Virol. 80, 1323-1337, 1999
A;Tille: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: 222020; MUID:99281911
A;Accession: T41857
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C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNRV
A;Variety: isolate T3
A;Variety: dolate T3
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
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A:Molecule type: DNA
A:Residues: 1-82 <KAM>
A:Cross-references: EMBL:L33180; PIDN:AAC63786.1
A:Experimental source: isolate T3
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 16:09:50; Search time 34.24 Seconds (without alignments) 46.364 Million cell updates/sec Run on:

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1 HQEGAMAVRLAGGLQKMVAL.....NTNVKFLAITTDCLQILAY 41 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 118-149 IN COMPLEX WITH
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MEDLINE=92376536; PubMed=1509266;
Butz S., Stappert J., Weissig H., Kemler R.;
Butz A., Stappert J., Water State H., Kemler R.;
Stappert Butz S., Stappert 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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Biochem. Biophys. Res. Commun. 268:243-248(2000).
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ilarity 97.6%; Pred. No. 6.5e-19;
Conservative 0; Mismatches 0
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Last annotation update)
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InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM0185; ARM; 11.
PR051TE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural 1
            entities requires a license agreement (
or send an email to license@lsb-sib.ch)
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                                                                                   EMBL; X87838; CAA61107.1; -.
                                                                                                       EMBL, 219054; CAA79497.1; -. PIR; S31988; S31988. PDB; 1G3J; 17-JAN-01. TRANSFAC; T02872; -.
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LEGURAL TRANSDÚCTION THROUGH THE WAT PATHWAY.

LEGURAL TRANSDÚCTION THROUGH THE WAT PATHWAY.

LEGURAL TRANSDÚCTION THROUGH THE WAT ALLOWS THE STIMULATION TO STUDIE FORM ALSO INTERACTS WITH APPC AND SECONDATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APPC AND SECONDATION. THE CYTOSOLIC FORM SINDS TCE/LEF.1 AND MAY ALSO BIND COMPINIS. AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATTENIN AND SECONDATION. CYTOPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF PROSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS STABLILIZED, (LOW LEVEL OF PHOSPHORYLATION).

CHEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS STABLILIZED, (LOW LEVEL OF PHOSPHORYLATION).

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CHEVEL OF DATAGONIZES THE ACTION OF GSK-3B. WINT-DEPENDENT ACTIVATION OF DATAGONIZES THE ACTION OF GSK-3B. WINT-DEPENDENT ACTIVATION OF DATAGONIZES THE ACTION OF GSK-3B. WINT-DEPENDENT ACTIVATION OF BEJA-CATENIN FAMILY.

CHEVEL OF DATAGONIZES THE ACTION OF GSK-3B. WINT-DEPENDENT ACTIVATION OF BEJA-CHERNIN SERIORES AND THE PROFILE IS NO LONGER DEGRADED,

RESULTING IN ITS ACCUMULATION IN CYTOPLASM.

CHEVEL OF DATAGONIZES THE ACTION OF GSK-3B. WINT-BEPRADES.

RESULTING IN ITS ACCUMULATION IN CYTOPLASM.

CHEVEL OF DATAGONIZES THE ACTION OF GSK-3B. WINT-BERGRADED,

RESULTING IN ITS ACCUMULATION IN CYTOPLASM.
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Pokütta S., Weis W.I.;
"Structure of the dimerization and beta-catenin-binding region of
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                                                                                                                                                                                                                                                                   J. Cell. Physiol. 181:258-272(1999).

-!- FUNCTION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN SIGNAL TRANSDUCTION THROUGH THE WIT PATHWAX (BY SIMILARITY).

-!- SUBUNIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND B-CADHERIN. THE MUCLEAR FORM BINDS TCF/LEF-1 AND MAY ALSO BIND PONTINS2 AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND ALSO FORM A TRIMBRIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORGE OF THE CADHERIN. MEDIATES THE ANCHORGE OF THE CADHERIN. MEDIATES THE ANCHORGE
                                                                                                                                                                                                      MEDLINE-99428593; PubMed-10497305; Chung S.S.W., Lee W.M., Cheng C.Y.; Study on the formation of specialized inter-Sertoli cell junctions in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CYTOPLASMIC WHEN IT IS UNSTABILIZED (HIGH LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS TABILIZED (LOW LEVEL OF PHOSPHORYLATION) (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN THE TESTIS.

DEVELOPMENTAL STAGE: HIGHLY EXPRESSED AT E30-60 DAY DPC IN THE TESTIS. REDUCED EXPRESSION AT E90 DAY DPC.

PTW. PROBABLY PHOSPHORYLATED BY GSK-3B. WNT-DEPENDENT ACTIVATION OF DVL ANTAGONIZES THE ACTION OF GSK-3B. PHOSPHORYLATION OF BETA-CATENIX IS REDUCED AND THE PROTEIN IS NO LONGER DEGRADED,

REGULTING IN ITS ACCUMULATION IN CYTOPLASM (BY SIMILARITY).

SIMILARITY: CONTAINS 12 ARM REPEATS.
                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9C29186B6DD54B87 CRC64;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                       STRAIN=SPRAGUE-DAWLEY; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6.7.6
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SMART; SM00185; ARM; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50176; ARM_REPEAT; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000225; Armadillo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF121265; AAD28504.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85454 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594
637
781 AA;
                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                     Beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                    CTNNB1.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions on any as its content is in no
                                                                                                                                                                                                                                                                                                                                                            GSCIENCE 254.1359-1361(1991).

- FINCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL
- ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
- PROTEINS. THE ASSOCIATION OF CATEXINS TO CAPHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
SERMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
PROPERTIES. ESSENTIAL COMPONENT OF THE VERTEBRATE WAT SIGNALING
- PATHWAY AND IS REQUIRED FOR FORMATION OF THE EMBRYONIC AXIS.
- SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                         McCrea P.D., Turck C.W., Gumbiner B.M.; "A homolog of the armadillo protein in Drosophila (plakoglobin) associated with E-cadherin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3ECD27232239F799 CRC64;
                           1 HOEGA-MAVRLAGGLOKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 192.5; DB 1
Pred. No. 6.5e-19;
); Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel.:22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01:MAR-2002 (Rel. 41, Last annotation update)
                                                                                                            781 AA
                                                                                                                                                                                                                                                                         1+1.
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                              Xenopus laevis (African clawed frog)
                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARM 2.
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ARM 5.
ARM 6.
ARM 7.
                                                                                                                                                                                                                                                                                                       MEDLINE=92073903; PubMed=1962194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfem; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M77013; AAA49670.1; -. PIR; S35099; S35099. HSSP. 00248; EMCAPP. TRANSFAC; TO3026; - INCEPPC; IPRO00225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Cell adhesion; Cytoskeleton; S
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                                                                                                             STANDARD;
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                                                                                                                                                                                                                                          Xenobns.
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Bestříogal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                    NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                  Beta-catenin,
                                                                                                                                                                                                                                       Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                             CINB_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE
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                                                                                             CTNB_XENLA
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Gaps

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Length 781; Indels

Score 192.5; DB 1; Pred. No. 6.5e-19;); Mismatches 0;

. 0

41; Conservative

Query Match Best Local Similarity Matches 41; Conserv

94.8%; 97.6%;

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ARM_MUSDO
Q02453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sir
Matches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformmatics and the BMIL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               "Identification of homologues to beta-catenin/plakoglobin/armadillo in two invertebrates, Urechis caupo and Tripneustes gratilla."; Biochim. Biophys. Acta 1173:337-341(1993).

-1- FUNCTION: BINDS TO THE CYTOPLASMIC DOWAIN OF THE CELL-CELL ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO CYHER (MEMBRANE) PROTEINS. THE ASSOCIATION OF CAFFININS TO CADHERINS PRODUCES A COMPLEX WHICH IS LINED TO THE ACTIN FILAMENT NETWORK, AND WHICH SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                             Trippeustes gratilla (Hawaian sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoskeleton; Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 HQEGSKMAVRLAGGLQKMVALLSRNNPKFLAITTDCLQILAY 322
265 HQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.0%; Score 170.5; DB 1;
85.7%; Pred. No. 7.6e-16;
11ve 3; Mismatches 2;
                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                        820 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L10354; AAA30089.1; -. PTR; S33794; S33794. HSSP, Q02248; 1DOW. HSSP, Q02248; 1DOW. Pfam; PF00514; Armadillo_seg; 12. Pfam; PF00514; Armadillo_seg; 12. PMSTE; SMORIE; PS50176; ARM_REPEAT; 9. Cell adhesion; Cytoskeleton; Structuc
                                                                        PRT;
                                                                                                                                                                                                                                                                   MEDLINE-93305730; PubMed-8318544; Rosenthal E.T.;
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                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             644
820 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                            Tripneustes.
NCBI_TaxID=7673;
                                                                                                                                                                                                                                                                                                                                                                                                                          PROPERTIES.
                                                                                                                                                  Beta-catenin.
                                                                        CTNB_TRIGR
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SEQUENCE
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                                           RESULT 5
CINB_TRIGR
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Muscoidea; Muscae; Musca.
                                                                                                                                                                                                                                                               "Identification of homologues to beta-catenin/plakoglobin/armadillo in two invertebrates, Urechis caupo and Tripneustes gratilla."; Blochim. Broches To Grief (MEMBRANE) PROTEINS TO GRIEF (MEMBRANE) PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                         Eukāryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
NCBL_TaxID=6431; .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
PR051TE; PS0176; ARM; REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 HQEGSKMAVRLAGGLQKMVLLLQRNNLKFLAITTDCLQILAY 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 7 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
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Last annotation update)
01.FEB-1994 (Rel. 28, Created)
01.FEB-1994 (Rel. 28, Last sequence update)
01.MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             813 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Armadillo segment polarity protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-93305730; PubMed-8318544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89070 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L10355; AAA30330.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26,
01-JUL-1993 (Rel. 26,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454
501
543
648
818 AA;
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                                                                                                                                                                                                                                                  Rosenthal E.T.;
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PRT;

STANDARD;

CTNB_URECA ID CTNB_URECA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                   housefly Musca domestica.";
J. 601. Evol. 36.224-233(1993)
-1- FUNCTION: SEGMENT POLARITY PROTEIN. MUTATION IN ARM PRIMARILY
AFFECT THE POSTERIOR PART OF THE SEGMENT AND LEAD TO THE
PRODUCTION OF ANTERIOR STRUCTURES WITHIN THIS REGION. MAY BIND
A CADHERIN AND PARTICIPATE IN THE TRANSMISSION OF DEVELOPMENTAL
         MEDLINE-93247062; PubMed-8483160;
Peifer M.A., Wieschaus E.;
"The product of the Drosophila melanogaster segment polarity gene
armadillo is highly conserved in sequence and expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                 Segmentation polarity protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.5%; Score 163.5; DB 1; Length 813; ilarity 81.0%; Pred. No. 7e-15; Conservative 3; Mismatches 4; Indels 1
                                                                                                                               -!- SUBCELLULAR LOCATION: INNER SURFACE OF CELL MEMBRANE.
-!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-!- SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73E61F59BDBFA580 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoskeleton; Structural protein.
1 48 ASP/GLU-RICH (ACIDIC).
221 ARM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARM_DROME STANDARD, PRT; 843 AA. P18824; 002371; 09W546; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Armadillo segment polarity protein. ARM OR EG:86E4.6 OR CG11579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                          ARM 2.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 9.
ARM 9.
                                                                                                                                                                                                                                                                             InterPro; IPR000255, Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89211895; PubMed-2707602;
                                                                                                                                                                                                                                                                                                                   PROSITE; PS50176; ARM_REPEAT; 9. Developmental protein; Segmentat Cell adhesion; Cytoskeleton; Str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88237 MW;
                                                                                                                                                                                                                                                              EMBL; L04874; AAA29292.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          813 AA;
                                                                                                                      INFORMATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=OREGON-R;
                                                                                                                                                                                                                                                                         002248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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**Nolecular nalysis of the armodillo locus: uniformly distributed
**Relear Dev. 136-1131959: A second D.**
**RELINE-982-995: PubMed-9633199; **Relear D.**
**RELINE-982-995: PubMed-9633199; **Relear D.**
**RELINE-982-995: PubMed-9633199; **Relear D.**
**RELINE-982-995: PubMed-10731133; **Relear D.**
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                                                                                                                                                                                                                                           SWART; SM00185; ARM; 11.
PROSITE; PS50176; ARM, REPEAT; 9.
Devolopmental protein; Segmentation polarity protein; Repeat;
Cell adhesion; Cytoskeleton; Structural protein; Phosphorylation;
                Peifer M., Pai L.-M., Casey M.; Phosphorylation of the Drosophila adherens junction
                                                                                                                                                                                                                                                                                                                                                                                            ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                 EMBL, AF001213; AAE58731.1; EMBL, AE021106; CAA15946.1; ALT_INIT. EMBL, AL021106; CAA15946.1; JOINED. EMBL, AL021086; CAA15946.1; JOINED.
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7.
7.
10.
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InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
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ARM
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          MEDLINE-95113174; PubMed-7529201;
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327
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REPEAT
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                                                                                                                                                                                                ä
   ARM 11.

ARM 12.

ARM 12.

ARM 12.

ARM 12.

ASP/GLU-RICH (ACIDIC).

ASP/GLU-RICH (ACIDIC).

LGPEEAYEGLYGGGPESVHSSHGGRAFHQGGYDTLPIDSMQ
GLEISSPVGGGAGGAPGNGGAYGGASGGGGNIGAIPPSGA
PTSPYSMDMDVGGTDAGALNFDLDAMPTPPNDNNNLAAWYD
TDC -> ILYO (IN NEUBAL ISOFORM).

WW. 40DADGFBB3163049 CRC64;
                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1: FUNCTION: COMMON JUNCTIONAL PLACUE PROTEIN. THE MEMBRANE-
-1: FUNCTION: COMMON JUNCTIONAL PLACUE PROTEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND EUNCTION
OF PORT THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE
THE STRUCTURE AND FUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE I
THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. SUBMILARITY: CONTAINS AT LEAST 9 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-92376536; PubMed-1509266;
Butz S., Stappert J., Welssig H., Kemler R.;
Plackglobin and beta-catenin: distinct but closely related.";
Science 257:1142-1144(1992)
                                                                                                                                                                                                  ij
                                                                                                                                                                  Score 163.5; DB 1; Length 843; Pred. No. 7.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSS0176; ARM REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Butz S.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                   01-071-1993 (Rèl. 26, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-MR*-2002 (Rèl. 41, Last annotation update)
01-0CT-1996 (Rèl. 41, Cosmoplakin III) (Fragment)
                                                                                                                                                                                                                                HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY
                                                                                                                                                                                                                                                                                                                                        621 AA
                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIK; S35092; S35092.
HSSP--002248; DD0W.
MGD; MGI:96650; Jup.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                      91152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M90365; AAB02885.1; -.
                                                                                                                                                                     Match
Local Similarity 81.0%;
es 34; Conservative 3
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                                                                                                                                                                                                                                                                                                                                          STANDARD;
      608
                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (Mouse):
                                                                                                                            843. AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
      585
648
718
718
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Q02257;
                                                                                                                      SEQUENCE
                      REPEAT
REPEAT
DOMAIN
VARSPLIC
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CAA47463.1;
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EMBL; x67078; ČAA47463.
PIR; S24636; S24636.
PIR; S35093; S35093.
HSSP; Q02248; 2BCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1; SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .. ASSOCIATED FORM
                                                                                                                                                                                                                                                                            Local Similarity
es 35; Conserv
                                                                                                                                                                                                                                   738. AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                           PLAK_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           JUP, OR DP3
                                             interPro;
                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE INTERNEDIATE JUNCTIONS SUGGESTS THAT IT PLAKS A CENTRAL ROLE IN THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-93093332; PubMed-1459359; Foughet B., Zimbelmann R., Franke W.W.; Identification of plakoglobin in oocytes and early embryos of Xenopus laevis: maternal expression of a gene encoding a junctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
ASSOCIATED FORM.
                                                                                                                                                                   ä
                                                                                                                                            Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The armadillo homologs beta-catenin and plakoglobin are differentially expressed during early development of Xenopus
                                                                                                                                                                   Indels
                                                                                                             17CF444607422BAA CRC64;
                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                       1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                             Score 161.5; DB 1;
                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III)
Xenopus laevis (African clawed frog).
                                                                                                                                                      Pred. No. 1e-14;
                                                                                                                                                                                                                                                                   738 AA
                                                                                                                                                                  Mismatches
              1.2.6.4.0.7.80
             ARM
ARM
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                                                                                                    ARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         plaque protein.";
Differentiation 51:187-194(1992)
                                                                                                                                                                 5;
                                                                                                             68111 MW;
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                                                                                                                                             79.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M95593; AAA49931.1; -.
                                                                                                                                                       83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Marais A.A., Moon R.T.;
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                            621 AA;
                                                                                                                                                       Best Local Similarity
                                                                                                                                                                 35;
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                                                                                               REPEAT
SEQUENCE
                                                                                                                                             Query Match
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PLAK_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE INTERNEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 common junctional plaque protein.";
proc.:Nell. Acad. Scl. U.S.A. 86.4027-4031(1989).
-!- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MENBRANE-
-!- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MENBRANE-
-!- SSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SÜBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89264555; Pubmed-2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
Schiller D.L., Cowin P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                  Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> V (IN REF. 2).
-> T (IN REF. 2).
569DBE69D08BBC58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 YOGGAKMAVRLADGLQKMVPLLNKNNPKFLAITTDCLQLLAY 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1-; SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HOEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 161.5; DB 1
Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Junction plakoglobin (Desmoplakin III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     > E
                                                                                                                                                                                                                                                                                                                                                                                                                         ARM 10
                                                                                                                                                                                                                                     ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 8.
                                                                                                                                                              ARM 1.
ARM 2.
ARM 3.
                                                                                                                                                 ARM
ARM
                        Pfam; PF00514; Armadillo_seg; 11
SMART; SM00185; ARM; 10.
                                                                                   PRÖSITE, PS50176, ARM REPEAT; 9
Cell adhesion, Cytoskeleton; St
IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequ
01-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81711 MW;
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
'14 EQKMVALLNKTNVKFLAI----TTDCLQI 38
                 REST : | TITELTE | 1:1|: | 33 EDNLELLERKTHIKEVAVMLNKKTTECLQL 62
                                                                                                                                                                                                                                                                                                 MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE007098; AAK46952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist; Rv2563; -. InterPro; IPR003838; DUF214. Pfam; PF02687; DUF214; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281
304
328
36025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 393:537-544(1998).
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
261
284
308
349 AA;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MT2639;
                                                                                                                                                                                                                                                                                      STRAIN-H37RV;
                                                                                                 YP63_MYCTU
Q50735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
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                                                             RESULT: 313;
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                             q
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possee R.D.;
                                                                                                                                                                                                                                                                                     2LA -> DSSL (IN REF. 1; AAA64895).
-> A (IN REF. 1; AAA64895).
472741F400D388FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R
"The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53.5; DB 1; Length 82;
Pred. No. 1.1;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                         62.1%; Score 126; DB 1; Length 743; 65.9%; Pred. No. 1e-09; live 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 9.5 kDa protein in HE65-PK2 intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                               protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9532 MW; 3303CBBDCB9175F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 255 YQEGAKMACAGRRAQKMVPLLNKNNPKFLAITTDCLQLLAY 295
                                                                                                                                                                                                                                                                                                                                                                                                                 1 HQEGAMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyhedrosis virus.";
Virology 202:586-605(1994).
-- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA
                                                                                  Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 10.
SMART; SM00185; ARM; 8.
PROSITE; PS50176; ARM_REPEAT; 8.
Cell adhesion; Cytoskeleton; Structural INIT_MET
       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     GQLA -> I
                                                                                                                                                                         ARM 1.
ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 6.
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                                                                                                                                                                                                                                                                                                                  81498 MW;
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                                EMBL; M23410; AAA64895.1;
PIR; A32905; A32905.
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 65.9
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
Matches 12; Conserv
                                               PIR; A32905; A32905
HSSP; Q02248; 2BCT.
MIM; 173325; -.
                                                                                                                                                                                                                                                                                                                  743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=46015,
                                                                                                                                                                                                                                             431
478
582
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Y120_NPVAC

Y120_NPVAC

P41673

Query Match

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SEQUENCE CONFLICT CONFLICT

REPEAT REPEAT REPEAT REPEAT

REPEAT

REPEAT REPEAT

REPEAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1. SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1. SIMILARITY: SOME, TO M.JANNASCHII MJ1507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Dobsoy R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A., Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s:
                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Devlin K., Feltwell T., Genles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Natter S., Seeger K., Skelton S., Squares S., Squares R., Skilston J.E., Taylor K., Whitehead S., Barrell B.G.; Peciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transmembrane; Signal; Complete proteome. SIGNAL 1 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. HYPOTHETICAL PROTEIN RV2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
694A971AC96A53F1 CRC64;
                                                        J50(32)
01-N0V-1997 (Rel. 35, Created)
15-7UL-1999 (Rel. 38, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 36.0 Kba protein Rv2563 precursor.
349 AA
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                                 ;;
                                                                                                                                                                                                     30-MAX-2000 (Rel. 39, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
01-MAX-2002 (Rel. 41, Last annotation update)
Potential phospholipid-transporting ATPase IK (EC 3.6.3.1) (Fragment).
ATP8B3 OR ATPIK OR FOS37502_2.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,

Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,

Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,

Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,

Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,

Kobayashi A., Olsen A.S., Carrano A.V.;

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + PHOSPHATE.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IV.
-!- CAUTION: REF.1 SEQUENCE DIFFERS AT SEVERAL POSITIONS FROM THAT SHOWN DUE TO DIFFERENCES IN THE PREDICTION OF SPLICE SITES.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00154; ATPASE_E1_E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Э
 DB 1; Length 349;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                15;
                                                            2 QEGAMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                               945 AA.
                6.8;
                                Mismatches
Score 52.5;
Pred. No. 6.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished observations (FEB-2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC004755; AAC17601.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001757; E1-E2_ATPase.
Pfam; PF00122; E1-E2_ATPase; 2.
PRINTS; PR00119; CATATPASE.
                          7;
25.9%;
37.5%;
                                Conservative
                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
           Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Transı
Multigene family
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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768
789
801
821
851
873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605866;
                                                                                                                                                                        A8B3_HUMAN
060423;
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TRANSMEM
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAING-CV. COLUMBLA,

SUCENCE FROM N.A.,

MEDLINE-21016719; PubMed-11130712;

MA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Minte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Minte O., Alonso J., Chen H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fulila C.Y.,

M. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Huizar L.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Rhan S., Khaykin E.,

M. Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A. Milischer J., Miranda M., Nuyeo M., Nierman W.C., Osborne B.I.,

Rangin G., Peterson J., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Otterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

M. Sequence and analysis of chromosome l of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Hagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL. REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE ARS CONSENSUS SEGUENCE (ACS) OF ORIGINS OF REPLICATION IN AN ATP-DEPENDENT MANNER (BY SIMILARITY).
--- SUBDUNT: ORC IS COMPOSED OF SIX SUBDUNTS (BY SIMILARITY).
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                 Gaps
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                                                                     PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                           DB 1; Length 945;
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                                                                                                                                                   2A28483C2F58D702 CRC64;
                                                     EXTRACELLULAR (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATIG26840 OR T2P11.3.
                                                                                                                                                                                                                                                                                                                                                                                                                    319 AA
                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                        505 GATALEDRLQDGVPETIKCLKKSNIKIWVLTGD 537
                                                                                                                                                                                                                               Pred. No. 23;
                                                                                                                                                                                                                                                                       4 GAMAV--RLAGGLQKMVALLNKTNVKFLAITTD 34
                 POTENTIAL.
                                                                                                                                                                                                         25.6%; Score 52; 36.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
                                   POLY-THR
                                                                                                                                                   MM;
                                                                                                                                                   107157
                                                                                                                                                                                                                           Best Local Similarity 36.4 Matches 12; Conservative
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                                                                       262.
711
715
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SEQUENCE
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DOMAIN
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Tue Jul 30 08:15:41 2002

EMBL; AC005508; AAD14490.1; -. Hypothetical protein; DNA-binding. SEQUENCE 319 AA; 36181 MW; 8573C6DD26206DE8 CRC64; SER

Query Match 25.4%; Score 51.5; DB 1; Length 319; Best Local Similarity 27.3%; Pred. No. 8.5; Matches 12; Conservative 11; Mismatches 10; Indels 11; Gaps

Search completed: July 29, 2002, 16:09:52 Job time: 757 sec

Dp δλ

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090424 brachydanio 09335 mus musculu 042486 gallus gall 061229 lytechinus 015151 homo sapien 09bwc4 homo sapien P70565 rattus norv 09114 ciona intes P79321 sus scrofa 09947 brachydanio 076152 ciona savig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9evr7 xenorhabdus
Q9vah2 drosophila
Q9x101 aythya amer
Q91w87 arabidopsis
                                                                          July 29, 2002, 16:12:02; Search time 124.4 Seconds (without alignments) 57.016 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                               US-09-641-104A-7
203
1 HQEGAMAVRLAGGLQKMVAL.....NKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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Q90335
Q42486
O61229
Q91851
Q91874
P70565
Q9144
P73321
Q9PVF7
Q9PVF7
Q9FVR7
Q9FVR7
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Q9FVR7
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_archeap:*
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sp_bacteria:*
sp_fung1:*
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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192.5
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156.5
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8
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Q9kkb3 rickettsia	о9ккв3	~	\leftarrow	24.4	., 49.5	45
Q91x99 arabidopsis	66X160	10	~	24.6	. 50	44
Q96143 homo sapien	096143	4	9	24.6	20	43
Q9vex8 drosophila	Q9VEX8	Ŋ	ŝ	₹.		42
	Q961R9	S	S	24.6	50	41
P74265 synechocyst	P74265		408	24.6		40
Q943x2 oryza sativ	Q943X2	10	c	₹.	. 50	39
staph	998660	16	æ	4	. 50	38
Q9vsh1 drosophila	Q9VSH1	S	240	24.6	20	37
4	Q9AB94	16	399	24.9	50.5	36
	Q9SSB7	10	370	24.9	0	35.
	069078	12	228	24.9	50.5	34
	09SSD5	10	920	25.1	51	33
	Q9CAA0	10	913	25.1	51	32.
	022266	10	526	25.1	51	31
Ø	Q9F5AB	N	422	25.1	. 51	30
	Q9ZZ28	æ	909	25:4	51.5	, 52
Q9x135 vidua chaly	Q9XL35		605	25.4	51.5	28
Q9sz64 arabidopsis	Q9SZ64	0	521	25.4	51.5	27
	Q9VM21	Ŋ	699	25.6	. 52	26.1
Q9fc35 streptomyce	Q9FC35	7	347	25.6	. 52	25
Q9jux7 neisseria m	Q9JUX7	16	190	25:6	. 52	24
Q910f9 adoxophyes	Q910F9	12	445	25.9	•	23 ,
. Q9v7q2 drosophila	09V702	'n	. 359	25.9	52.5	22
	004250	10	571	26.1	53	21
Q9hzq7 pseudomonas	Q9HZQ7	16	379	26.1	53	50
	Q9JZW3	16	190	26.1	53	19.
Q9h0c0 homo sapien	0Эн60	4	505	26:4	٠	18.
O92476 bombyx mori	092476	12	82	26.4	. 753.5	17 1 1
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ALIGNMENTS

RESULT

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							Craniata; Vertebrata; Euteleostomi;	Euteleostei; Ostariophysi;							th occu									. 4	:	Length 780;	Indels				
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	780 AA.	_	sequence update)	annotation update)		a dani	ata; 1							.T.;	axis									PRACE		192.5	No. 2		AITID	AITTDO	
	PRT;	Created)	Last se	Last an		(Zebr	Crani	releos	nio.				127;	Moon R	ryonic	tenin.				uup.	ċ	12.				Score 192.5;	Pred. No. Z.1e-18; 0: Mismatches 0		TNVKFL	I I I I I I TNVKFL	
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	PRELIMINARY;	(TrEMBLrel.	TrEMBLrel.	Lrel.		(Zebra	; Chor	optery	rinida				PubMed	lmaz.	conda	of . be	273(19	9732.1		526-36	5; Arm	adillo	M; 11	ARM_RI			vat		GLOKM	GLOKM	
	PRELIM	(Treme	(Treme	(Tremburel.		Brachydanio rerio (Zebrafish) (Zebra danio).	Eukaryota; Metazoa; Chordata;	Actinopterygii; Neopterygii; Teleostei;	Cypriniformes; Cyprinidae; Danio.	955;		SECUENCE FROM N.A.	MEDLINE-96122902; PubMed-8562427;	Kelly G.M., Erezyilmaz D.F., Moon R.T.;	"Induction of a secondary embryonic axis	the overexpression of beta-catenin.";	Mech., Dev. 53:261-273(1995).	EMBL; 041081; AAC59732.1;	HSSP; 1935222; 1G3J.	ZFIN; 2DB-GENE-980526-362; ctnnb.	InterPro; IPR000225; Armadillo.	Pfam; PF00514; Armadillo_seg;	85; AF	50176; 7			Best Local Similarity 97.0 Matches 41: Conservative		1. HOEGA-MAVRLAGGLOKMVALLNKTNVKFLAITTDCLQILAY	HQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY	
		,	-1996	-2001	NTN	danio	ota; M	pteryg	iforme	axID=7		CE FRO	E-9612	G.M.,	tion o	erexpr	Dev. 5	U41081	P35222	ZDB-GE	ro; IP	PF0051	SMOOT	E; PS5		ch ,	1 Simi 41:		QEGA-M	OEGAKM	
· /`	090424	090424; 01-NOV-1996	1-NOV	OI-DEC-ZOOI	B-CATENIA. CTNNB:	rachy	ukary	ctino	yprin	CBILT	 T	ECCEN	EDLIN	elly.	Induc	he ov	lech.	MBL;	SSP;	FIN;	nterP	fam;	MART;	PROSITE;		Query Match	hes		.⊞ 12:	264 H	
090424	a.	DI DI			SN C									_		_	. ,							SOR	X	One	Matc		Qy	qq	

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Gaps

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090335

RESULT 090335

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SEQUENCE FROM N.A. ...
MEDITINE-98104237; Pubmed-9441670;
Miller J.R., McClay D.R.;
"Changes in the pattern of adherens junction-associated beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                Score 192.5; DB 13; Length 781;
Pred. No. 2.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 821;
                                                                                               chicken beta-catenin.";
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71E21D562A99C5AD CRC64;
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6D205D9A4DBAC562 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 HOEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accompany morphogenesis in the sea urchin embryo.";
Dev. Biol. 192:310-322(1997).
EMBL; U34814; AAC06340.1; -.
HSSP: Q02248; IDOW.
                                                                                                                                                                                                                                                                                                                                                                                                                             265 HQEGAKMAVRLAGGLOKMVALLNKTNVKFLAITTDCLQILAY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 1 HQEGA-MAVKLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 166.5; DB 5;
Pred. No. 9.9e-15;
3; Mismatches 3;
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PROSITE: PSS0176; ARM_REPEAT; 8.
SEOUENCE 821 'AA,' 89558 WW; 71E21D562A99C5AD C
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                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                  STRAIN-WHITE LEGHORN, TISSUE-DORSAL SKIN, MEDITINE-97464066; Pubmed-9322759, LINE, LINE, LINE, Wildelltz R.B., TISSUE, And Cond. C.M. Widelltz R.B., TISSUE toon and congecterization of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002086; Aldehyde_dehydr.
Interpro; IPR000225; Armadillo.
Pfdm; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 12.
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                                                                                               General 196:201-207(1997).
EMBL: 1082964; AAB80856.1; -.
HSSP: P35222; 16334.
Interpo: IPR000225; Armadillo.
Pfan: PF00514; Armadillo.seg; 12.
                                                                                                                                                                                                                                      PSS0176; ARM_REPEAT; 8
781, AA; 85438 MW;
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01,
17,
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity, 97.68;
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01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
DUENCE FROM N.A.
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Q15151; Q15093;
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Arakawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
R. Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
R. Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R. Feischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
R. Kohil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
R. Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
R. Baka J., Boffelli D., Bolinga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
R. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Wasaki H., Zato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wyonshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wasaki W.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Functional amoutation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK018515; BAB31250.1; -.
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                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE COLON CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 9030417H18, FULL INSERT SEQUENCE.
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Pfam, PF00514; Armadillo_seg; 12.
SMART, SM00185; ARM, 12.
PROSTIE; PS50176; ARM_REPEAT; 7.
SEQUENCE 781 AA; 85546 MW; 937538C3B5CD75D1 CRC64;
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Last annotation update)
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MEDLINE-21085660; PubMed-11217851;
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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Best Local Similarity
Matches 41; Conserv
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                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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NCBI_TaxID-9031;
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"Molecular cloning and sequencing of the rat plakoglobin cDNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC000441; AAH00441.1; -. EMBL; BC011865; AAH11865.1; -.
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases:
EMBL: U58858; AABD6317.1;
HSSP: Q02248; 2BCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; 8.
PR051TE; PS00176; ARM_REPEAT; 7.
SEQUENCE 745 AA; 81777 MW; 9E2F52910A7ACD41 CRC64;
                                                                                                                                       7.
34DF7BFB4748BCF4 CRC64;
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01.FEB-1997 (TrEMBLrel. 02, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Best Local Similarity 83.3%; Pred. No. 4.5e-14;
Matches 35; Conservative 2; Mismatches 4
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STRAIN=SPRAGUE-DAWLEY; TISSUE=VAGINA;
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                                                         HSSP; (002248; 2BCT:
InterPro; IPR000225; Armadillo.
Pfam; PP00514; Armadillo_seg; 11.
SMART; SM00185; ARM; 12.
PROSITE; PS50176; ARM, REPEAT; 7.
SEQUENCE 745"AA; 81726 MW; 34
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01-FEB-1997
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                                                                                           SEQUENCE FROM N.A.
MEDLINE-89264555; PubMed-2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
Schiller D.L., Cowlin P.;
"Molecular cloning and amino acid sequence of human plakoglobin, the common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989).
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whittock N.V., Eady R.A.J., McGrath J.A.; "Genomic Organization and amplification of the human plakoglobin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
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3519A0973748BCF4 CRC64;
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EMBL; D50808; BAA05435.1; --
EMBL; AF306723; AAG16727.1; --
EMBL; AF233882; AAG16727.1; JOINED.
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SEQUENCE FROM N.A.
TISSUE-PLACENTA, CHORIOCARCINOMA;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. 118:836-840(1995).
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SEQUENCE 745 AA; 81744 MW;
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01-JUN-2001 (TrEMBLrel. 17,
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TISSUE=LUNG CARCINOMA;
Strausberg R.;
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tes 35; Conserv
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Query Match

Matches

Q9BWC4 9

RESULT O9BWC4

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A SEQUENCE FORM N.A.

MEDILINE-88443204; PubMed-9769178;

A Yoshida S., Marikawa Y., Satoh N.;

Yoshida S., Marikawa Y., Satoh N.;

T Requiation of the trunk-tail patterning in the ascidian embryo: a

T Regulation of cascades between lithium/beta-catenin and

T localized maternal factor pem.";

Dev. Biol. 203:264-279(1998).

I Dev. Biol. 203:224: 1634.

R EMBL; AB012160; BAA32789.1; -

R EXEP: P35222; 1634.

R Interpro; IPR000255; Armadillo.

R Fran, PF005144, Armadillo.seg; 11.

R SMART; SM00185, ARM; 9.

R SMART; SM00185, ARM; 9.

R SGUENCE 773 AA; 85217 MW; C1340CF82AFEBDAB CRC64;
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona.
NCBI_TaxID=51511;
                                                                                                       SEQUENCE FROM N.A.:
MEDLINE-9386700; Publed-10456847;
MEDLINE-9386700; Publed-10456847;
Cerda J., Reidenbach S., Pratzel S., Franke W.W.;
"Cadherin-catenin complexes during zebrafish oogenesis: heterotypic junctions between coocytes and follicle cells.";
Biol. Reprod. 61:692-704 (1999).
EMBL; AF099738; AAD56592.1;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophyai; Cypriniformes;:Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                          77.1%; Score 156.5; DB 13; Length 729; 78.6%; Pred. No. 2.2e-13; tive 4; Mismatches 4; Indels 1;
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ZFIN; ZDB-GENE-991207-22; jup.
InterPro; IPR000225; Armadillo.
Pfan; PR00514; Armadillo_seg; 11.
.SMAR; SM00185; ARM, 8.
PROSITE; PS50176; ARM_REPEAT; 8.
SEQUENCE 729 AA; 80033 MW; 91E00417B4FD8CEE CRC64;
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Matches 35; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                               Inal K., Takada N.A.

Imal K., Takada N., Satoh N., Satou Y.;
Imal K., Takada N., Satoh N., Satou Y.;

"An essential role of beta-catenin in the endoderm specification of ascidian embryo.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB03143; BAA92185.1;

HSSP; PS35222; IG3J.

InterPro; IPR000225; Armadillo.

Pfam; PF00514; Armadillo_seg; 11.

PROSITE; PS50176; ARM EMBRAT; 6.

SEQUENCE 769 AA; 84703 MW; F61CC489B436E1BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TSSUB-SMALL INFESTINE;
Winterce A.K., Fredholm M.;
"Evaluation and characterization of a porcine small intestine CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                      Query Match 79.1%; Score 160.5; DB 5; Length 769; Best Local Similarity 83.3%; Pred. No. 6.4e-14; Matches 35; Conservative 2; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 284131; CAB06327.1; -
HSSP; P35222; 1G3J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73F7CCF3B917A41A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-Mar.1997 (TrEMBLrel. 03, Created)
01-Mar.1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BETA CATENIN (FRAGMENT).
Sus Scrofa (Plg).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 
NCBI_TaxID-9923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MX-2000 (TrEMBLrel. 13, Created)
01-MX-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL-ADHESION PROTEIN PLAKOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            255 HQEGAKEAVRLAGGLQKMVYLLSRDNVKFLAIDTDCLQILAY 296
                                                                                                                                                                                                                                                                                                                                                                                                        1 HQEGAM-AVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.3%; Score 157; DB 6; 18est Local Similarity 100.0%; Pred. No. 2.3e-14; Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 729 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LAGGLOKMVALLNKTNVKFLAITTDCLOILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO00225; Armadillo.
Pfam; PF00514; Armadillo_seg; 2.
PROSITE; PS50176; ARM_REPEAT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA; 12717 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                   NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
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P79321;
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RESULT P79321

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Adams M.D., Cedniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Cedniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Cedniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E. Li P.W., Hoshins R.A., Galle R.F.,
RA Gocoge R.A., Lewis S.E., Hichards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Marchas F.G., Champe M., Pfeiffer B.D.,
RA Man.K.H., Doyle G., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I.,
RA Cherry J.M., Cawley S., Dahner M., Dew I., Diez S.M.,
RA Cherry J.M., Cawley S., Dahner M., Diedar S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahner M., Diegar S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dannes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Godson K., Deup L.E., Downes M., Dugan R.A., Burtis N.C., Harvis M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Alalali M., Kaliah F., Krapfe G., Krayitz S., Kulp D., Lai Z.,
Alalali M., Kaliah F., Krapfe G., Krayitz S., Kulp D., Lai Z.,
RA Moutte S.M., Wolther E., Workey M., Strong R., Nelson D.L.,
RA Moutte S.M., Wolth W., Wurphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Moutte S.M., Wolth W., Wurphy B., Murphy L., Murny D.M., Nelson D.K.,
Ra Margarolo M., Pittman G.S., Pan S., Pollard J., Purl, Wang Z.,
Ra Spier E., Spradling A.C., Stapleton M., Strong R., San E.,
Ra Shieb B.C., Siden Klames E.W., Sungers R., She H., Wang Z.-Y., Wang S., Cabor Y., Wang S., Chill D., Shen H.,
Rang Z.-Y., Wassarman D.A., Wainstock G.M., Weigsenbach J.,
Rang S.M., Woodage T., Wolly W., C., Wu D., Yang S., Yao Q.A.,
R. The genome sequence of Drosophila melanogaster.";
R. The genome sequence of Drosophila Melanogaster.";
R. The 
                                                                                            Dřóšophila melánogaster (Fruit fly).
Bukaryota, Metazoa: Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.6%; Score 56; DB 5; Length 959; Best Local Similarity 34.3%; Pred. No. 38; Matches 12; Conservative 6; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108922 MW; AEB5C6FA21A19627 CRC64;
         01_JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QEGAMAVRLAGGLQKMVALLNKTNVKFLAITTDCL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607
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                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00514; Armadillo_seg; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000225; Armadillo.
InterPro; IPR000210; BTB_POZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BTB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 959 AA;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50097;
                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
                                                                                                                                                                                            Ephydroidea; Dro
                                         CG7837 PROTEIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; 1
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9XL01
Q9XL01;
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         DD BREEF BRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Xenorhabdus.
                                                                                                                                Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                   Hobmayer E., Hatta M., Fischer R., Fujisawa T., Holstein T.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morgan J.A.W., Ousley M., Ellis D., Jarrett P., "Novel toxins from Xenorhabdus strains with activity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.1%; Score 57; DB 2; Length 1660; llarity 33.3%; Pred. No. 51; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AJ296651; CAC19493.1; -- SEQUENCE 1660 AA; 185738 MW; AFABEA20AD70B164 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nematodes.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                689E5E982CD5051A CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HQEGA-MAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAY 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.6%; Score 153.5; DB 5; Best Local Similarity 81.0%; Pred. No. 6.5e-13; Matches 34; Conservative 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suglyama T.;
"Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadillo gene family.";
Gene 172:155-159(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GAMAVRLAGGLQKMVALLNKTNVKF -- LAITTDCLQILA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-WILDTYPE 105;
MEDLINE-96257271; Pubmed-8654977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nssr; Q02246; 2BC1.
InterPro; IPR00025; Armadillo.
Pfam: PF00514; Armadillo_seg; 10.
SMART: SM00185; ARM; 10.
PROSITE; PS50176; ARM_REPEAT; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U36781; AAC47137.1; -. HSSP; Q02248; 2BCT.
                                                                                         Hydra magnipapillata (Hydra)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16,
16,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEMATICIDAL PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kenorhabdus bovienii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      806 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=40576;
                                                                                                                                                         Hydridae; Hydra.
NCBI_TaxID=6085;
                                                            BETA-CATENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001
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Best Local Simi
Matches 13;
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09EVR7;

Q9EVR7 RESULT 13

Q9EVR7

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SEQUENCE

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Gaps

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Q9VAH2; Q9VAH2

HARE

RESULT 14 Q9VAH2

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MEDLINE-98424473; PubMed-9751919; MEDLINE-9842473; PubMed-9751919; Johnson K.P., Sorenson M.D.; "Comparing molecular evolution in two mitochondrial protein coding genes (cytochrome b and ND2) in the dabbling ducks (Tribe: Anatini)."; Mol. Phylogenet. Evol. 10:82-94(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Interordinal relationships of birds and other reptiles based on whole mitochondrial genomes.";
Syst. Biol. 48:138-152(1999).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98393707; PubMed=9724766;
Mindell D.P., Sorenson M.D., Dimcheff D.E.;
Mindtiple independent origins of mitochondrial gene order in birds.";
Proc. Natl. Acad. Sci. U.S.A. 95:10693-10697(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorenson M.D., Dimcheff D.E., Ast J.C., Yuri T., Mindell D.P.; "Complete mitochondrial DNA sequences for flive birds and a turtle."; submitted (SEP-1998) to the EMBJ/GenBank/DDBJ databases.

-1. CATALIYIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Mindell D.P., Sorenson M.D., Dimcheff D.E., Hasegawa M., Ast J.C.,
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Aythya.
NCBI_TaxID=30385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20113882; PubMed=10649633;
Sorenson M.D., Cooper A., Paxinos E.E., Quinn T.W., James H.F.,
Olson S.L., Fleischer R.C.;
"Relationships of the extinct moa-nalos, flightless Hawaiian
waterfowl, based on ancient DNA.";
Proc. R. Soc. Lond., B. Biol. Sci. 266:2187-2193(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00662; oxidored_q1_N; 1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 607 AA; 66508 MW; 1D37736075BE8A09 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001750, Oxidored_q1.
Interpro; IPR001516; Oxidored_q1_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00361; oxidored_q1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF090337; AAD32262.1;
                                                                                Aythya americana (Redhead).
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                    Mitochondrion
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11; 27.3%; Score 55.5; DB 8; Length 607; 40.0%; Pred. No. 26; Live 2; Mismatches 8; Indels 1. Query Match
Best Local Similarity 40.0°
Matches 14; Conservative

4 GAMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQI 38 ò g

353 GEQDIRKMGGLQKM------LPVTTSCLTI 376

Search completed: July 29, 2002, 16:12:04 Job time: 474 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 29, 2002, 16:07:53 ; Search time 158.47 Seconds

(without alignments)
30.139 Million cell updates/sec

US-09-641-104A-8

212 1 GNÇESKLIILASGGPQALVN.....TYTYEKLLMTTSRVLKVLSV Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
7: /SIDSI/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
7: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
8: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
9: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
11: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
12: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
13: /SIDSI/gcgdata/hold-geneseqy-embl/AA1993.DAT:*
14: /SIDSI/gcgdata/hold-geneseqy-embl/AA1993.DAT:*
15: /SIDSI/gcgdata/hold-geneseqy-embl/AA1993.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy-embl/AA1994.DAT:*
17: /SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
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20: /SIDSI/gcgdata/hold-geneseqy-embl/AA1998.DAT:*
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20: /SIDSI/gcgdata/hold-geneseqy-embl/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseqy-embl/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseqy-embl/AA1998.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:* A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

				•								
	Description	Human beta-catenin	Human beta catenin	Human beta-catenin	Novel human secret	Human beta-catenin	Mouse beta-catenin	Novel human secret	Human beta-catenin	Drosophila melanoq	Drosophila melanog	Drosophila melanog
	ID		AAB07290	AAY70740	AAU28118	AAE06038	AAE06039	AAU28306	AAY33234	ABB60196	-	-
	DB	20	21	21	22	22	22	22	20	22	22	22
	Length	43	781	781	781	781	781	800	43	840	840	840
ф	Query ore Match Length DB I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.6	87.7	87.7	87.7
	Score	212	212	212	212	212	212	212	209	186	186	186
	Result No.	1	7	e	4	Ŋ	9	7	æ	თ	10	11

700 957 957 1003 22 1004 22 1004 22 128 22 24 25 26 26 26 26 26 26 26 26 26 26	
2003 2003	AAG33365 AAG93071 AAB79594 AAR48726 AAW02698
112	

ALIGNMENTS

AAY33219 standard; peptide; 43 AA. AAY33219; AAY33219 RESULT

(first entry) 18-NOV-1999 Human beta-catenin protein armadillo repeat arm5 fragment.

Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; modulator; interaction domain; transcription factor; TCF-4; oncogenic; tunor'suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; Wrt signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth.

Homo sapiens.

DE19909251-A1.

26-AUG-1999.

99DE-1009251 22-FEB-1999; (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

98DE-1007390

21-FEB-1998;

Von Kries J; Birchmeier W,

WPI; 1999-470389/40.

Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor

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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the armadillo domain (arm units 3-8) of beta-catenin, and mutants of the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or E-cadherin; and (C) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin is a key compound in the Wht signalling pathway and is involved in development of tumors. Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic. (A) which inhibit interaction are particularly used to treat tumors, specifically carcinoma of the colon and melanoma, but also, where they promote interaction, to simulate regeneration of organs and issues, specifically hair growth. AAY33217-Y33222 represent human beta-catenin armadillo repeat fragments described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense compounds targeting nucleic acids encoding human beta catenin (HBC) useful for treating diseases associated with HBC expression and as prophylaxis to prevent or delay infection, inflammation or tumor formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta catenin; cadherin; metastasis; cadherin-associated protein; human; colorectal cancer; melanoma; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 212; DB 20; 100.0%; Pred. No. 4.2e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB07290 standard; Protein; 781 AA.
                                    Disclosure; Page 7; 16pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0344519
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suppressor gene products
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N-PSDB; AAA58320.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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Gaps

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Example 13; Columns 45-52; 35pp; English.

Example 13; Columns 45-52; 35pp; English and Example 15; Colored 15; Color
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a method of female primate contraception comprising administering an antagonist of a wnt polypeptide, inhibiting occyte development. Wnt polypeptides are useful for promotive maturation of an immature occyte. Wn polypeptides are also useful for increasing the number of mature occytes and to enhance occyte viability. Soluble fragments of wnt polypeptides have the ability to inhibit wnt signalling, e.g., by blocking binding of a naturally-occurring wnt protein to its receptor. They may be used to generate monoclonal antibodies which can inhibit occyte development. The present sequence is the human beta-catenin protein. Dominant negative mutants of beta-catenin lack one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contraceptive composition for inhibiting oocyte development in a female primate comprises a wnt polypeptide antagonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 212; DB 21;
100.0%; Pred. No. 1.8e-22;
vative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mchahon AP, Parr BA; Vaino S;
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Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200021555-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency, SCID; autoimmune disorder; allory; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
or more armidillo-like repeats which participate in cadherin binding. Other mutants include those lacking amino acids 555-781 or 424-781,
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n F, Ma Y, Zhou
Xue AJ, Wang J;
                                                                                                                                                           ö
                                                                                                                       Score 212; DB 21; Length 781;
Pred. No. 1.8e-22;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F,
Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue
                                                                                                                                                                                                          43
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                                                                                                                                                                                           1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secretory protein, Seq ID No 287.
                                                                                                                                                           0; Mismatches
                                                                                                                       100.0%; Score 212; 100.0%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple sclerosis; rheumatona artnrifertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                               AAU28118 standard; Protein; 781
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; 2000US-0616847.
; 2000US-0665363.
; 2000US-0693267.
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2000US-0574454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-2001; 2001WO-US04942
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                    or 1-422 of beta-catenin.
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-589934/66.
                                                                                                                                     Best Local Similarity
Matches 43; Conserv
                                                                  781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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19-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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17-JUN-2000;
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                                                                      Sequence
                                                                                                                        Query Match
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the polypeptide as well as for studying modulators of the polypeptides.

(1) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, certification's disease, Huntington's disease, and amyotrophic lateral solerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopolesis and is useful for treating myeloid or lissue growth, and in tissue repair, healing of burns, inclisions, or itsue growth, and in tissue repair, healing of burns, inclisions, of treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for cepertusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections; autoimmune disorders e.g. multiple sclerosis, reactions; autoimmune disorders e.g. multiple sclerosis, reactions and conditions, such as asthma or other respiratory problems. In about the conditions, such as asthma or other respiratory problems. In about the conditions, such as asthma or other respiratory problems.
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                                                                                                                                                                                                                                                                                                                                                                                        fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In witro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 100.0%; Score 212; DB 22; 100.0%; Pred. No. 1.8e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE06038 standard; Protein; 781 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signalling pathway; beta-catenin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta-catenin protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 -JAN-2001; 2001WO-US01459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781 AA;
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beta-catenin in the cell

us-09-641-104a-8.rag

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mammalian stem or progenitor cells, which comprising increasing the mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell in an in vitro culture medium for a period sufficient for the progenitor or stem cell to divide. The number of cells having the functional penotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoietic function to autologous or allocation. Beta-catenin is a pivotal player in the signalling pathway in this protein. Beta-catenin is a pivotal player in the signalling pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoletic function; allogeneic recipient; signalling pathway; beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In vitro expansion of mammalian stem or progenitor cells, useful for producing 'cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels beta-catenin in the cell .
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 212; DB 22;
100.0%; Pred. No. 1.8e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
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              Disclosure; Page 23-24; 33pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse beta-catenin protein #2.
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N-PSDB; AAD11165.
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Matches 43; Conserv
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                    oristin vitro culture medium for a period sufficient for the progenitor oristen cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their plutipotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoietic function to autologous or allogeneic recipients. The present sequence is mouse beta-catenin protein, as a pivotal player in the signalling pathway initiated by wit proteins, which are mediators of several developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SciD; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Wehrman T, Ren F, Ma Y, Zhou
Zhang J, Chen R, Xue AJ, Wang J;
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                                                                                                                                                                                                                                                                                                                           Length 781;
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                                                                                                                                                                                                                                                                                                                             100.0%; Score 212; DB 22;
100.0%; Pred. No. 1.8e-22;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secretory protein, Seq ID No 663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU28306 standard; Protein; 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MXY-2000; 2000US-0574454.
17-UUN-2000; 2000US-0596193.
14-JUL-2000; 2000US-0616847.
19-SEP-2000; 2000US-0665363.
20-OCT-2000; 2000US-0693267.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-2001; 2001WO-US04942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 43; Conservative
2001-589934/66.
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Yang Y,
                                                                                                                                                                                                                                                                             Sequence 781 AA;
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                                                                                                                                                                                                                                                processes.
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Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor

suppressor gene products

(DELB:) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

Birchmeter W, , Von. Kries J;

WPI; 1999-470389/40.

Agents

, 98DE-1007390.

21 FEB-1998;

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intransmentory contituency, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling (1), (11) and modulators of (11) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptides. (I) induces the proliferation of neural cells and regeneration of neural cells and regeneration of nerve partinson's disease, Huntington's disease, and amyotrophic lateral cells in addition, (I) is involved in chemotactic or chemokinetic cells. In addition, (I) is involved in chemotactic or chemokinetic cells. In addition, (I) is involved in chemotactic or chemokinetic cells. In addition, (I) is involved in chemotactic or chemokinetic or lymphoid cell disorders, platelet disorders such as thrombocytopenia to Insue growth, and in tissue repair, healing of burns, incisions, culcers, for treating osteoporosis, osteoarthitis, bone degenerative cell disorders, or periodontal disease. Furthermore, (I) is also useful for continuous and treatment of lung or liver fibrosis, or moreful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rhemmatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects blorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth; mutant.
                                             invention relates to novel isolated human secreted polypeptides (I) polynucleotides (II). (I) and (II) are useful for treating lammatory conditions such as arthritis, nephritis, Crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1;
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100.0%; Pred. No. 1.9e-22;
ive 0; Mismatches 0;
Example 2; SEQ ID No 663; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid sequences of the invention.
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                                                The invention relates
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Best Local Similarity
Matches 43; Conserv
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99DE-1009251.

22-FEB-1999;

26-AUG-1999

DE19909251-A1,

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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tunor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the armadillo domain (arm units 3-8) of beta-catenin, and mutants of the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or E-cadherin; and (C) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin beta-catenin (A) which interaction with LEF-1 or TCF-4 is development of tumors. Generally its interaction with LEF-1 or TCF-4 is ontogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic (A) which inhibit interaction are particularly used to treat tumors, especially carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate ergemeration of organs and tissues, specifically half growth. AAY3330+Y33241 represent mutant the method of the colon and melanomy but also, the colon and elements described in the method of the colon and melanomy but also, the colon and melano
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Pred. No. 1.2e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB60196 standard; Protein; 840 AA
                                                                                                                                                                                                                                                              Example 4; Fig 5; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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1; Mismatches
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                                                                                                                                                                     87.78;
88.48;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                          Matches: 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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                                                                                                                                                                                Best Local Similarity
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                                                                                                                                     840.AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical
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                                                                                                                                                                                                                                                                            RESULT 1
ABB65821
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                                                                                                                                                                                                                  (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                 solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0156-ABL30511), expressed DNA sequences (ABL011676-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                Disclosure; SEQ ID NO 7380; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                              Length 840;
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                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 24249.
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                                                                                                                                                                                                                                                                                                                                                            1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                       Score 186; DB 22,
                                                                                                                                                                                                                                                                                                                        Pred. No. 1.46
1; Mismatches
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            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB65819 standard; Protein; 840 AA.
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            PWD,
                                                                                                                                                                                                                                                                                                              87.7%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                    New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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            Venter JC, Adams M,
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                                   2001-656860/75.
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                             840 AA;
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                                               N-PSDB; ABL04299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical.
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                                                                                           interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB65819;
                                                                                                                                                                                                                                                                               Sequence
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                           1.8
(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at (Itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell. interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                Length 840;
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        312 gnqeskliilasggpnelvrimrsydyekllwttsrvlkvlsv 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 24255.
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                                                                                                                                                                                                                                                                                                                                                                                                                    . 3:1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
                                                                                                                                                                                                                                                                                                                                Score 186; DB 22;
Pred. No. 1.4e-18;
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Query, Match
                                                                                                                                               RESULT 13.
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                                         Best Loca
Matches
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                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The ligand pref. includes a fragment indicated in the features, or the total protein. The ligand pref. contains only a single BS and has an amino acid sequence <100 (pref. <20) residues in length. The ligand may also comprise a plurality of fragment 389..394. A therapeutic compsn. contg. the polypeptide is used to stimulate or inhibit Blymphocyte proliferation in patients with B cell lymphoma. Blymphocytes and myeloma's can be stimulated in patients with immunodeficiencies and immunoglobulin secretion by hybridoma cultures can be boosted.

The compsn. can be administered to inhibit infection in vitro or in vivo by Epstein Barr Virus.
                                                                                                                                                                                                                                                                                             auto-immune disease;
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                                      Length 840;
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA segment encoding CR-2 ligand and CR2 binding site treat auto-immune disease, B-cell lymphoma and inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                          385..400
/note= "fragment pref. inlcuded"
389..394
/note= "fragment most pref. included"
                                                                                                          43
                                                                                         1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
                                                                                                                                                                                                                                                                                                                                                                       300..312
/note= "fragment pref. included"
                                       Score 186; DB 22;
Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                         Cellular receptor 2; CR2; binding site; BS; au
Epstein-Barr Virus; EBV; B lymphocyte; ligand.
                                                                  . 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 303..309
/note= "fragment most
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                   AAR11354 standard; Protein; 700 AA.
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                                      87.78;
88.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epstein-Barr virus infection
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89US-0404679
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                                                                                                                                                                                                                                                                Cellular Receptor 2 ligand
                                                                                                                                                                                                                                      03-JUN-1991 (first entry)
                                                                  Conservative
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                                      Query Match
Best Local Similarity
840 AA
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Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lernhardt W;
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                                                                38;
                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Sequence
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                                                                Matches
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700 AA;

Seguence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis. hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. alzabimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food preparations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to 29 human secreted proteins. The
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Length 700;
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Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 957;
                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food.
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Score 114; DB 12;
Pred. No. 5.3e-08;
1; Mismatches 2;
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Birse CE,
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                                                                                                                                                                                                                                                                                                                                               Secreted protein encoded by gene #4
                                                                                                       272 lvgimrnysyekllwttsrvlkvlsv 297
                                                                                                                                                                                                                           Ą.
                                                                                43
                                                                                18 LVNIMRTYTYEKLLWTTSRVLKVLSV
                                                                                                                                                                                                                       AAB80374 standard; protein; 957
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Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
53.8%;
llarity 88.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-2000; 2000WO-US19735.
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Best Local Similarity 28.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-123261/13.
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             957 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2001
                                        23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                 AAB80374;
                         Local
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Pred. No. 47;

Similarity' '28.6%;

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Query Match

DB 21; Length 1003;

Score 55;

25.9%;

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Best Loc
Matches
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                                                                                                                                                                                                                                                            Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; neotropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; strocytal disorder; anglogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; plastocoelic disorder; epithelial disorder; commander; blastocoelic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory disorder; immunologic disorder
                                                                                                                                                                                 Human PRO290 protein sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 61; Fig 4; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0143048.
99US-0145698.
99WO-US28313.
99WO-US30911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36-JAN-2000; 2000WO-US00376
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-572270/53.
N-PSDB; AAC58368.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200053755-A2
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1999;
02-JUN-1999;
23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1999;
                                                                                            29-JAN-2001
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             AAB24058;
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Godowski PJ;
                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted and transmembrane protein; PRO; cytostatic;
cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes human secreted and transmembrane PRO
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, specific cells, to cause targeted cell death -
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
ROY, MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
    14; Indels
                                                                                                                                                                                                                                                                                                                                                                  Human, PRO290 (UNQ253), protein sequence SEQ ID NO:33.
                                | Corporation | 
    Mismatches
                                                                                                                                                                                                                 rd; Protein; 1003 AA
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    12;
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2000WO-US07377
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                                                                                                                                                                                                                                                                                                                     (first entry)
12; Conservative
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N-PSDB; AAF44100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic assay
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11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
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15-MAR-2000;
20-MAR-2000;
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01 DEC-1999;
16 DEC-1999;
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05-JAN-2000;
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08-OCT-1999
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20-JUL-1999
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                                                                                                                                                                                                AAB65162
                                                                                                                                                                         RESULT
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proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as can be used for targeted delivery of bioactive molecules, such as sequences, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents: The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR prinars and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF4259 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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Sequence 1003 AA;

1; 4; Gaps Ouery Match 25.9%; Score 55; DB 22; Length 1003; Best Local Similarity 28.6%; Pred. No. 47; Matches 12; Conservative 12; Mismatches 14; Indels 4

1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLS 42 ò

qq

Search completed: July 29, 2002, 16:07:54 Job time: 644 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 29, 2002, 16:05:08; Search time 57.6 Seconds (without alignments) 18.234 Million cell updates/sec Run on:

212 1 GNQESKLIILASGGPQALVN.....TYTYEKLLWTTSRVLKVLSV US-09-641-104A-8 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

Title:

231628 seqs, 24425594 residues Searched:

231628

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ion		7. 4	12,	e 13, Appl	26,	5,	e 5, Appli	'n	4	e 4, Appli	4	e 4, Appli	4	4	7	7	7	e 2, Appli	5,	7	20,	7,	7	7	~	e 10, Appl	47,
Description	endembes	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-08-740-223A-14	-08	US-08-740-223A-12	US-08-740-223A-13	US-08-740-223A-26	US-09-351-457-5	US-09-561-500-5	US-09-561-108-5	US-08-373-579-4	US-08-418-595-4	US-08-665-926-4	US-08-348-492-4	US-09-162-437-4	US-08-740-223A-4	US-08-373-579-2	US-08-418-595-2	US-08-665-926-2	US-08-348-492-2	US-09-162-437-2	-740-223A	US-08-740-223A-20	US-09-351-457-2	US-09-561-500-2	US-09-561-108-2	US-08-750-717-2	US-08-982-785A-10	US-08-118-270-47
% Query Match Length DB	497 4	478 4	4 90 4	491 4	495 4	495 4	495 4	495 4	497 1	497 2	497 2	497 2	497 4	497 4	498 1	498 2	498 2	498 2	498 4	498 4	498 4	498 4	498 4	498 4	3898 4	620 4	347 1
% Query Match 1	27.8	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	24.5	24.1	23.6
Score	59		54.5	54.5	٠	٠		54.5								54.5		54.5	54.5	54.5	54.5	54.5	54.5	54.5	52	51	20
Result No.		7	m	4	Ŋ	9	7	σο	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

	Sequence 47, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 6, Appli	Seguence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 5, Appli	Sequence 8, Appli	Sequence 11, Appl	Sequence 21, Appl	Sequence 44, Appl
	PCT-US93-08528-47	US-09-110-517-2	US-08-876-991-2	US-09-059-853-2	US-08-804-439A-17	US-08-720-229-17	US-08-381-936-2	US-08-943-374-2	US-08-019-870-1	US-08-019-870-6	US-07-747-901A-3	US-07-935-312-3	US-08-019-870-3	US-08-019-870-5	US-08-019-870-8	US-08-019-870-11	US-08-314-309A-21	US-08-633-760-44
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	23.6 : 347	22.6 : 1581	22.6 +3898	22.6 3898	22:4 . 849	22:4 849	22:2415	22.2 415	22.2 :: 5773	22:2 773		22:2 : . 774			Ť	22.2 774	22.2 774	22.2 774
ls.	28. 7. 11 50	29 1117 48	30 71:1 48	31 15 4 48	32; 4: 47.5	33 11:47.5	34 47	35 47	36 47	37 100 47	38: 1: 47	39.14. 47	40 7. 47	41: 47	42 - 47	43 47	44 47	45 47

ALIGNMENTS

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Sequence 14, Application US/08740223A
Sequence 14, Application US/08740223A
Batent No. 6.265564
GENERAL INFORMATION:
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STREET: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
CORENTING SYSTEM: DOS
SOFTWARE: FastESEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-0CT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CODERT, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COCATION: 1...497
COTHER INFORMATION: mouse TIE-2 ligand US-08-740-223A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,108
PFR: REG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COBET, ROBER J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                             TELEFRX: 914-345-7/4-
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
TENGTH: 497 amino:acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: mTL1
US-08-740-223A-14
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Query. Match

27.8%; Score 59; DB 4; Length 497;

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Sequence 13, Application US/08740223A
Sequence 13, Application US/08740223A
Sequence 13, Application US/08740223A
Sequence 13, Application US/08740223A
Sequence 13, Application September 1
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
TITEE OF INVENTION: Intercellular Signalling Molecule NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query, Match 25.7%; Score 54.5; DB 4; Best Local Similarity 42.5%; Pred. No. 4.6; Matches 17; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill Road
                                                            ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LUCATION: 1...490
; OTHER INFORMATION: human TIE-2 ligand 1
US-08-740-223A-12
                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-0CT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-NGG-1996
ATTORNAY AGENT: INFORMATION:
NAMM: CODERT, ROBERT J
REGISTRATION NUMBER: 35,108
REGISTRATION NUMBER: 35,108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 emino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Diskette
IBM Compatible
                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 777 Old CITY: Tarrytown
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                                 Gaps
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                                 Indels
                                                                                                                                                                                                                      Sequence 7, Application US/08740223A
Patent No. 6265564
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches 11;
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                                                                                                    2 NQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKV 40
           Pred. No. 0.99;
                             5; Mismatches
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CODERT, ROBERT J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEFAX: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
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; Sequence 12, Application US/08740223A
; Patent No. 6265564
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OTHER INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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Best Local Similarity 42.5%;
Matches 17; Conservative
           41.0%;
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APPLICANT: Davis, et al.
TITLE OF INVENTION: Expr
           Best Local Similarity 41.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Tarr
STATE: NY
                                                                                                                                                                                   RESULT 2
US-08-740-223A-7
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Length 490;
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APPLICANT: Philip E. Thorpe
APPLICANT: ROIf A. Brekken
TITLE OF INVENTION: ANTHONY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT FILING DATE: 2000-04-28
PRIOF FILING DATE: 60/131,432
PRIOF FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: THORPE, PHILIP E.
APPLICANT: TITLE OF INVENTION: CANCEN TREATMENT METHODS USING THERAPEUTIC CONJUGATES
TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
FILE REFERENCE: 4001.002300
CURRENT APPLICATION NUMBER: US/09/351,457
CURRENT APPLICATION NUMBER: US/09/351,457
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VET: 2.0
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Pred. No. 4.7;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                 Length 495;
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                 Score 54.5; DB 4;
Pred. No. 4.7;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                          151 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 184
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                                                                                                                                                                                                                                                                                                                                                                       2 NOESKLIILASGGPOALVNIMRTYTYEK-LLWTTSRVLKV 40
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                                                                                                                                                     NAME/KEY: 2N1C1F (chimera 4)
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Best Local Similarity, 42.5%;
Matches 17; Conservative
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    495 amino acids
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Matches 17; Conservative
                                            single
                                                                                        MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-351-457-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo saptens
US-09-561-500-5
                                                                                                                                                                         LOCATION: 1..495;
CTHER INFORMATION:
US-08-740-223A-26
                                                               linear
                          TYPE: amino acid
STRANDEDNESS: si
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LENGTH: 495
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US-09-561-500-5
    LENGTH:
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Patent No. 6265564
GENERAL IMPORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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STREET: 777 Old Saw Mill Road
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chicken TIE-2 ligand 1
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Pred. No. 4.7;
5; Mismatches
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APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: FASTEM VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR ADDITOR:
APPLICATION NUMBER: US/08/740,223A FILING DATE: 25-OCT-1996 CLASSIFICATION: 536
                                                                                                                                               NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
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REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REC
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 42.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                    LENGTH: 491 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 1...491
; OTHER INFORMATION:
US-08-740-223A-13
                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: ChTL1
                      FILING DATE: 25 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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STATE: NY
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US-08-740-223A-26
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Sequence 4, Application US/08418595
Sequence 4, Application US/08418595
Sequence 4, Application US/08418595
Sequence 4, Application US/08418595
SEQUENCE 4, Application THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Regeneron Pharmaceuticals, Inc.
STRED: 777 Old Saw Mill River Road
CITY: Tarryton
STRED: ADDRESSE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.7%; Score 54.5; DB 1; Length 497; 42.5%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
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APPLICATION NUMBER: 105 08/373,579
PILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR: APPLICATION UNDERE: US 08/348,492
PRIOR: APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
APPLICATION NUMBER: US 08/330,261
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATE: 07-OCT-1994
PRIOR APPLICATION DATE: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT: NEORMATION:
NAME: CODET: RODET J.
REGISTRATION: NUMBER: 36,108
REGISTRATION: NUMBER: 36,108
REGISTRATION: NUMBER: 36,108
RELEPAX: (914):345-740
IRELEPAX: (914):345-771
INFORMATION FOR SEQ.ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acids
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APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-0CT-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: . US/08/418,595 FILING DATE: 06-APR-1995 CLASSIFICATION: . 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIDLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 42.55
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-373-579-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 10591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10.
US-08-418-595-4
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APPLICANT: POLINE Thorpe
APPLICANT: POLINE Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERBENCE: 400.1002584
CURRENT APPLICATION NUMBER: US/09/561,108
CURRENT PILING DATE: 2000-04-28
PRIOR FILING DATE: 10999-04-28
NUMBER OF SEQ ID NOS: 44
SOUTHWARE: PATENTIAN VEF. 2.0
SEQ ID NOS: 44
SEQ ID NOS: 44
SEQ ID NOS: 44
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                                                                                                                      Gaps
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Sequence 4, Application US/08373579

Sequence 4, Application US/08373579

Patent No. 565041004:

PAPLICANT: Davis, et al.

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54.5; DB 4; Length 495; Pred. No. 4.7; 5; Mismatches 11; Indels
                                                         DB 4; Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRECTION OF STREET: 77/ OLC
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: TBM FC compatible
COMPUTER: TBM FC compatible
COMPUTER: TSM FC compatible
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 184
                                                                                                                                                                                                                               151 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                                                                                                                                                      2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                  Score 54.5; DB Pred. No. 4.7; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09561108
Patent No. 6342221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.7%;
milarity 42.5%;
Conservative 5,
                                                      Query Match 25.7%;
Best Local Similarity 42.5%;
Matches 17; Conservative
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US-09-561-108-5
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Best Local Similarity
Matches 17; Conserv
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Gaps
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                                                                              APPLICANT: Davis et.al.
TITLETOF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES TITLETOF INVENTION: THEREOF NUMBER OF SEQUENCES: 4
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence: 4, Application US/09162437
Patent No. 6166185
GENERAL: UNFORMATION:
GENERAL: DAVIS: et al.
TITLE: OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE: OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,492
FILIMO DATE: 02-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 NOTSRLEI ------OLLENSLSTYKLEKOLLQOTNEILKI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NOESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The state of the s
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road CITY: Tarrytown. STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54.5; DB
Pred. No. 4.7;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-CCT-1994
PRIOR.APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REG 330B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10591
COMPUTER READABLE:FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence.4, Application.US/08348492
Patent No. 5879672
GENERALINFORMATION:
APPLICANT: Davis, et.al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 347-7000
TELEFAX: (914) 347-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.7%;
Best Local Similarity 42.5%;
Matches 17; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 113:
US-09-162-437-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
ADDRESSER: Regeneron Pharmaceuticals, Inc.
STREET: 777 old Saw Mill River Road
CITY: Tarrytown
CITY: Tarrytown
STREET: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TARRORDELE FORM:
COMPUTER:
COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.5; DB 2; Length 497;
Pred. No. 4.7;
5; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54.5; DB 2;
Pred. No. 4.7;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
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NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEFONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08665926
Patent No. 5851797
GENERAL INFORMATION:
                                       TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 antino acids
TYPE: amino acids
TOPOLOGY: linear
    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.7%;
Best Local Similarity 42.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.7%;
Best Local Similarity 42.5%;
Matches 17; Conservative
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LENGTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-418-595-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-665-926-4
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-665-926-4
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E: Floppy disk IBM PC compatible

COMPUTER:

RESULT 12 US-08-348-492-4

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Gaps
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Sequence'2, Application US/08373579
Patent'No. 5550490
GENERAL'INFORMATION:
APFLICANT DA'LS; et al.
TITLE OF INVENTION: THEREOF
TUMBER OF SEQUENCES: 6
CORRESSONDER ADDRESS:
CORRESSONDER ADDRESS:
ADDRESSEE: Reqeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 17-JAN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 NQTSRLEI------QLLENSLSTYKLEKQLLQQTNEILKI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54.5; DB
Pred. No. 4.7;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
FRION'APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR'APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
FRIOR APPLICATION DATA:
                      USSN 60/022/999
                 APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-0406-1996
ATTORNEY AGENT INFORMATION:
NAME: CODERT, ROBERT J
REGISTRATION'NUMBER: 36.108
REFERENCE/DOCKET NUMBER: REG 333
TELECHOME: 914-345-7400
TELEPHONE: 914-345-7400
ITELEPHONE: 914-345-7701
INFORMATION FOR SEQ'ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Human TIE-2 ligand 1; LOCATION: 1..2146; OTHER INFORMATION: from T98G clone US-08-740-223A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/319,932 FILING DATE: 07-0CT-1994 ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.7%;
Best Local Similarity 42.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                          ESS: single
linear
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Tarrytown
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15.
US-08-373-579-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.7%; Score 54.5; DB 4; Length 497; Best Local Similarity 42.5%; Pred. No. 4.7; Matches 17; Conservative 5; Mismatches 11; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4. Application US/08740223A

Patent No. 6265564

GENERAL INFORMATION:
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
    SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPERATING SYSTEM: DOS
SOFTWARE: FastESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT 1996
CLASSIFICATION: 536
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
FILING DATE: 17-AN-1995
FILING DATE: 17-AN-1995
FILING DATE: 09-DEC-1994
PRIOR APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION NUMBER: US 08/348,492
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/30,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/30,261
FILING DATE: 10-OCT-1994
PRIOR APPLICATION NUMBER: US 08/310,261
FILING DATE: 10-OCT-1994
ATTORNEY AGENT: NFORMATION:
ANAME: COLOUT DATE: TANDER TO NAME: US 08/319,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
                           SOFTWARE: Patentin Release #1.0, 'CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTERISTICS:
LULH: 497 amino acids
TYPE: amino acids
TOPOLOGY: 11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-162-437-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10591
COMPUTER READABLE FORM:
                                                                                                                         CLASSIFICATION:
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REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUTCATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEPHONE: (914) 345-7721
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-373-579-2
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Gaps Ouery Match
25.7%; Score 54.5; DB 1; Length 498;
Best Local Similarity 42.5%; Pred. No. 4.7;
Matches 17; Conservative 5; Mismatches 11; Indels ò g

Search completed: July 29, 2002, 16:05:09 Job time: 479 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 29, 2002, 16:09:11; Search time 70.63 Seconds (without alignments) 58.500 Million cell updates/sec Run on:

US-09-641-104A-8 212 1 GNQESKLIILASGGPQALVN.....TYTYEKLLWTTSRVLKVLSV 43 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	beta-catenin - hum	1	beta-catenin - Afr	ā		plakoglobin - mous	hypothetical prote	armadillo segment	plakoglobín - Afri	beta-catenin - Hyd	armadillo protein	beta-catenin - Cae	hypothetical prote		oliqopeptide trans	hypothetical prote	ABC transport syst		hypothetical prote		VPS9 protein - yea	hydrolase - Deinoc	hypothetical prote	probable homeodoma	host cell factor 1	qenome polyprotein	polyprotein - hog	hypothetical prote	probable oligopept
SUMMARIES	ID	A38973	S35091	835099	533794	A32905	S35092	533793	T12689	535093	JC4835	T43175	T23341	B72672	T37631	C98207	AF3079	AI2139	G90576	T28696	C69879	S49629	A75406	D90166	C84732	T43277	S57437	S58295	G75354	F95949
	DB	7	~	7	7	~	~	7	~	7	7	~	~	~	7	7	7	~	7	7	7	~	7	~	~	7	7	7	~	7
	Length	781	781	781	820	744	621	817	843	738	908	811	678	364	811	307	307	293	842	170	214	451	222	405	721	782	3898	3898	66	307
ФP	Query	100.0	100.0	98.1	92.0		٠.	89.6	87.7	87.3	82.1	42.9	37.0	27.1	26.9	26.7	26.7	26.4	25.9	25.7	25.5			24.5			24.5	24.5	24.3	24.3
	Score	212	212	208	195	194	190	190	186	185	174	91	78.5	57.5	57	56.5	56.5	26	52	54.5	54	54	52	25	52	52	52	52	51.5	51.5
	Result No.	-	7	m	4	S	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

F44B9.1 protein - hypothetical prote	polyhedrin - Bomby hypothetical prote	ylucose o phosphac VACB protein - yea hypothetical prote	hypothetical prote unknown protein T5	regulatory protein 26s proteasome req	probable protein k hypothetical prote	probable ubiquitin hypothetical prote	competence-damage
S44807 S74037	PYNVNV E84155	144845 S50446 G86445	C84609 H96803	S64903 S67156	T43420 B90281	T50325 A81926	B97340
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761	241	578	2048	1082	584	585	411
24.3	24:1	24.1	24.1	23.8	23.6	23.6	23.3
0 . 51.5	3751	51.	37 . 51	9 : 50.5	1. 50	3 . 50 4 . 49.5	5 49.5

ALIGNMENTS

- human beta-catenin

C.Species: How sapiens (man)
C.Species: Mono Sapiens (man)
C.Species: Mono Sapiens (man)
C.Species: J6-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 08-Oct-1999
C.Date: 26-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 08-Oct-1999
C.Accession: A38973; S55356; S31988
R.Huelsken, J.; Birchmeier, W.; Behrens, J.
J. Cell Biol. 127, 2061-2069, 1994
A?Title: E-cadherin and APC compete for the interaction with beta-catenin and the cyt
A; Accession: A38973; MUID: 95105247
A; Accession: A38973; MUID: 95105247
A; Accession: A38973; MUID: 95105247
A; Residues: 1-781 <HUE>
A; Reference number: S55356
A; Description: H. sapiens beta-catenin mRNA.
A; Reference number: S55356
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-781 <NOL>
A; Cross; references: EMBL: X87838; NID:q1154853; PIDN:CAA61107.1; PID:g860988
C; Comment: The cytoplasmic protein beta-catenin normally binds to a region in the cyt

C;Comment:.Cellular levels of beta-catenin are regulated in part by the adenomatous p d cancerous cell growth.
C;Genetics:

A;Gene: GDB:CTNNB1; CTNNB A;Cross-references: GDB:141922; OMIM:116806 A;Map postition: 3P22-3p21.3 C;Keywords: apoptosis; carcinogenesis; cell adhesion; cytosol F;151-676/Region: 40-residue repeats

ö Length 781; Indels 100.0%; Score 212; DB 2; llarity 100.0%; Pred. No. 6.1e-21; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 43; Conserv

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Gaps

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Dp

RESULT 2.
\$35091 ...
beta-catenin - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (c;Pacces: Musculus (c;Pac

307 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 349

Dp ò

beta-catenin - African clawed frog

1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 43

100.0%; Score 212; DB 2; 100.0%; Pred. No. 6.1e-21; iive 0; Mismatches 0;

43; Conservative

Query Match Best Local Similarity Matches 43; Conserv

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$33793 | https://docum.com/protein-isponworm (Urechis caupo) | hypothetical protein-isponworm (Urechis caupo) | c;Species:Urechis caupo | c;Species:Urechis caupo | c;Species:Urechis caupo | c;Species:Urechis caupo | c;Species:Urechis | caupo | c;Species:Urechis | c;
                                                                                                                                                                                                                                                                                                                        R. Frankers, W. W.; Goldschmidt, M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cow-
Proc. Natl. Acad. Sci. U.S.A. 86, 4027-4031, 1989
A.Titler Molecular clooning and amino acid sequence of human plakoglobin, the common J
A. Reference; Molecular clooning and amino acid sequence of human plakoglobin, the common J
A. Reference; A32905; MUID:89264555
A) Accessing preliminary
A; Molecular clooning and A; Molecular clooning acid sequence of human plakoglobin, the common J
A; Restugi preliminary
A; Molecular clooning acid sequence of human plakoglobin, the common J
A; Molecular clooning acid sequence of human plakoglobin, the common J
A; Restugi preliminary
A; Molecular clooning acid sequence of human plakoglobin, the common J
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C;Date: 222 Nov-1989 #sequence_revision 22-Nov-1989 #text_change 29-Aug-1997
C;Accession: A32905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297. GNQESKLIILANGGPQALVQIMRNYSYEKLLMTTSRVLKVLSV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 GNOESKLILANGGPOGLVQIMRNYSYEKLLMTTSRVLKVLSV
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Pred. No. 5.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March 1915%; Score 194; DB 2; Local Similarity, 90.7%; Pred. No. 1.7e-18; S9; Conservative 2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: Robb:JUP
A; Cross, references: GDB: 126565; OMIM: 173325
A; Map position: 7 Pter-7qter
C; Reywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.6%;
88.4%;
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A;Molecule type: mRNA
A;Residics: 1-621 <BUT>
A;Cross,references: EMBL:M90365
C;Keywords: cytoskeleton
                                                                                                                                                              - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 38; Conservative
                                                Best Local Similarity
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A; Molecule, type: mRNA
A; Residues!: 1-817 <ROS>
                                                                                                                                                                   plakoglóbin, desmosomal;
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Best Local Si
Matches, 39;
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C;Species: Tripneustes gratuilla
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C;Cacession: S33794
C;Acession: Biophys. Acta 1173, 337-341, 1993
A;Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver
A;Reference number: S33793, MUID:93305730
A;Accession: S33794
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-820 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Nanopus laavis (African clawed frog)
C; Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C; Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C; Accession: S35099
R; Accession: S35099
A; Title: A homolog of the armadillo protein in Drosophila (plakoglobin) associated with A; Title: A homolog of the armadillo protein in Drosophila (plakoglobin) associated with A; Accession: S35099
A; Molecule type: mRNA
A; Residences: GB: M77013; NID: G214020; PIDN: AAA49670.1; PID: G214021
C; Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                             R;Butz, S.; Stappert, J.; Weissig, H.; Kemler, R.
Science 257, 1142-1144, 1992
A;Title: Plakoglobin and beta-catenin: distinct but closely related.
A;Title: Plakoglobin and beta-catenin: distinct but closely related.
A;Tatle: S15091, MUD:92376536
A;Status: S2091, MUD:92376536
A;Status: preliminary
A;Molecule type: mRNA
A;Status: 1-781 - KBUT>
A;Cross-references: EMBL:M90364; NID:g192141; PIDN:AAA37280.1; PID:g192142
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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307 GNOESKLIILASGGPQALVNIMRTYSYEKLLWITSRVLKVLSV 349

QQ

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1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV

Query Match

98.1%; Score 208; DB 2;
Best Local Similarity 97.7%; Pred. No. 2.2e-20;
Matches 42; Conservative 1; Mismatches 0

hypothetical protein - sea urchin (Tripneustes gratilla)

43

RESULT

qq

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323 GNQESKLIILASGGPAALVHIMRTYDYEKLLWTTSRVLKVLSV 365

1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 43

Score 195; DB 2; Pred. No. 1.4e-18; 1; Mismatches 2

92.0%; ilarity 93.0%; Conservative

Query Match Best Local Similarity Matches 40; Conserv

us-09-641-104a-8.rpr.

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Page

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armadillo protein homolog BAR-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Ta-1000 *sequence_revision 11-Jan-2000 *text_change 18-Feb-2000
C;Accession: T43175; T28813;
R;Eisenmann, D.M.; Maloof, J.N.; Simske, J.S.; Kenyon, C.; Kim, S.K.
submitted to the EMBL Data Library, May 1998
A;Bescription: The beta-catenin homolog BAR-1 and LET-60 Ras coordinately regulate th
A;Reference number: Z22328
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Reterence number: EMBL:AF063646; PIDN:AAC17424.1
R;Minx, M.
Submitted to the EMBL Data Library, January 1996
A;Description: The sequence of C. elegans cosmid C54D1.
A;Reference number: Z20527
A;Reference number: Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyaccesiston: JC4835
R; Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T.
Gene 172, 155-159, 1996
A; Title! Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadill
A; Reference number: JC4835; MJID: 96257271
A; Status: nucleic acid sequence not shown
A; Molecule: type: mRNA
A; Residues: 1-806 < HOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:U36781; NID:g1407600; PIDN:AAC47137.1; PID:g1407601
C;Comment: This protein plays roles in cadherin-mediated cell adhesion and in signal
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: X
A;Introns: 23/2; 65/3; 97/3; 132/3; 181/3; 223/2; 261/3; 332/3; 414/3; 452/3; 500/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-811 <MIN>
A;Cross-references: EMBL:U46673; PIDN:AAC48154.1; GSPDB:GN00028; CESP:C54D1.6
A;Experimental source: strain Bristol N2; clone C54D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JC4835.47 beta-catenin - Hydra magnipapillata

C;Species::Hydra magnipapillata

C;Date::15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                             Gaps
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                                                                                                                                          Length 738;
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A;Crossireferences: EMBL:X67078; NID:g65252; PID:g65253
C;Keywords: cytoskeleton
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                                                                                                                                                                                                                                                                             "11" GNOESKLIILASGGPOALVNIMRTYTYEKLLWTTSRVLKVLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 174; DB 2;
Pred. No. 1.1e-15;
3; Mismatches 4
                                                                                                                                             DB 2;
                                                                                                                                          Score 185; DB 2;
Pred. No. 3e-17;
1; Mismatches
                                                                                                                                          87.3%;
86.0%;
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83.7%;
                                                                                                                                                                             Best Local Similarity 86.09
Matches 97; Conservative
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Best Local Similarity 83.7
Matches 36; Conservative
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A;Gene: betaCtn
                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT .10.
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C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Man-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S35093; S24636
A;Title: Identification of plakeglobin in oocytes and early embryos of Xenopus laevis: mA;Reference number: S35093; MUID:9309332
A;Reference number: S35093
A;Accession: S35093
A;Accession: S35093
A;Residues: 1-738 cFOUP
A;Residues: SEMBL:M95593; NID:9214656; PIDN:AAA49931.1; PID:9214657
A;Reference number: S24636
A;Reference number: S24636
A;Reference number: S24636
A;Reference number: S24636
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R; Riggleman, B.; Wieschaus, E.; Schedl, P.
Genes Dev. 3, 96-113, 1989
A; Title: Molecular analysis of the Armadillo locus: uniformly distributed transcripts
A; Reference number: A31861; MUID:89211895
A; Accession: A31861
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                                                                                                                                                                                                                                                                                                                                                                  Mighten segment polarity protein - fruit fly (Drosophila melanogaster)
Mightenate names: protein 8684.6
C:Species: Drosophila melanogaster
C:Species: Drosophila melanogaster
C:Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C:Accession: T12689; A31861
R:Ferraz, C: Vidal, S: Brun, C: Bucheton, A: Demaille, J.G.
submitted to the EMBL Data Library, January 1998
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: 21757
A:Reference number: 21757
A:Reference number: 21757
A:Reference number: 2188B:ALD21106; MID:e1371406; PID:e1249776; PIDN:CAA15946.1
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                                                                             Gaps
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C;Genetics:
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Pred. No. 2.5e-17;
       Length 817;
                                                                      Indels
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                                                                                                                                                                             330 GNQESKLIILASGGPGELVRIMRSYTYEKLLWTTSRVLKVLSV
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                                                                                                                                   1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
   Score 190; DB 2;
Pred. No. 6.9e-18;
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A;Molecule type: mRNA
A;Residues: 133-184,'V',186-225,'T',227-292 <DEM>
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                                                                   1; Mismatches
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A;Cross-references: FlyBase:FBgn0000117
A;Introns: 11/1; 557/3; 624/3; 715/3; 748/1
A;Note: 86E4.6
C;Keywords: cytoskeleton
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88.48;
   89.68;
90.78;
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Best Local Similarity 88.4*
Matches 38; Conservative
                                                                      Conservative
                        Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-843 <RIG>
   Query Match
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Using peptide transport system permease protein oppB AGR_L_1206 [imported] - Agrobacte C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C; Accession: C98207
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 233-2328, 2001
A; Itile: Genome Sequence of the Plant Pathogen and Blotechnology Agent Agrobacterium A; Reference number: A97359; PMID:11743194
A; Accession: C98207
A; Residues: Pathogen and Blotechnology Agent Agrobacterium A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Accession: T37631.
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: 1-811 < BRO>
A STATUS = STATUS =
                                                                                                                                                                                                                     probable execyst complex component - fission yeast (Schizosaccharomyces pombe) C.Species; Schizosaccharomyces pombe C.Species; Schizosaccharomyces pombe C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C.S.Cocession: 137631 R.Brown, 10:; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
                                        173 GSREFDAIIVAAGPWTGFISGLQALSNMLRVYRCEALI 210
1 GNQESKLIILASG-----GPQALVNIMRTYTYEKLL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26: LMRFAPGGPENLERPLPPQTMENLMRTYHLDEPLW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 3GKPQTLMDFFRTNNHDKMLLCAQRTRQLLAL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 SGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57;
Pred. No.
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Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: 221733
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A; Gene: AGR_L_1206
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Matches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: B72672
R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Tamaka, T.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn A; Reference number: A72450; MUID:99310339
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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      Length 811;
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45.0%; Pred. No. 0.012;
ative 10; Mismatches 11;
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   Score 91; DB 2;
Pred. No. 0.00029;
9; Mismatches 15
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Pred. No. 4.8;
7; Mismatches
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A; Introns: 14/1; 235/1; 290/1; 620/3
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1 Similarity 39.5%;
15; Conservative
      Query Match 42.9%;
Best Local Similarity 41.5%;
Matches 17; Conservative
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Best Local Similarity 45.0%
Matches 18; Conservative
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A; Residues: 1-364 <K
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us-09-641-104a-8.rpr

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OM protein - protein search, using sw model

July 29, 2002, 16:09:52; Search time 34.24 Seconds (without alignments) 48.626 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-641-104A-8 212 1 GNQESKLIILASGGPQALVN.....TYTYEKLLWTTSRVLKVLSV

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

G	P35.22 homo sapien 00.2248 mus musculu 09w48 rattus norv P26.33 xenopus lae P35.23 tripreustes P149.23 homo sapien 00.2257 mus musculu P35.24 urechis cau 00.2453 musca domes P188.4 drosophila P30.99 xenopus lae 0.3546 rattus norv 0189.20 bos taurus 0.089.30 homo sapien 0.089.30 homo sapien 0.089.30 homo sapien 0.089.30 pseudomonas P34.22 caenorhabdi 09rmc acinetobact P39.96 saccharomyc P19.263 saccharomyc P19.2455 human herpe P3.3897 protecus mir 09uze8 Pyrococcus 01.771 caenorhabdi P7.749 buchnera ap
SUMMARIES	CTNB_HUMAN CTNB_MOUSE CTNB_XRAT CTNB_XRAT CTNB_XRAT CTNB_XRAT CTNB_TRIGR PLAK_HUMAN PLAK_MOUSE CTNB_URECA ARP_LUSDO ARM_DROME PLAK_XBNIA AGP1_BOVIN AGP1_BOVIN AGP1_BOVIN AGP1_HUMAN AGP1_BOVIN AGP1_HUMAN AGP1_BOVIN AGP1_BOVIN AGP1_BOVIN AGP1_BOVIN AGP1_BAST CHRA_PERAF AGP1_BOVIN AGP1_HOWAN AGP1_BOVIN AGP1_HOWAN AGP1_BOVIN AGP1_AGTIM VASS YEAST RCRI_YEAST RCRI_YEAST RCRI_YEAST RCRI_XCRE RCRI_YEAST RCRI_XCRE RCR_ RCR_ RCR_ RCR_ RCR_ RCR_ RCR_ R
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Q15648 h peroxisom	Q07878 saccharomyc	P19712 hog cholera	002739 bos taurus	P48595 homo sapien	P57448 buchnera ap	P38206 saccharomyc	P56518 strongyloce	051578 borrelia bu	P40979 caldicellul	P38616 saccharomyc	Q46654 erwinia amy	
PPRB_HUMAN	VP13_YEAST	POLG_HCVA	PTI6_BOVIN	SB10_HUMAN	AMPA_BUCAI	RFT1_YEAST	HDA1_STRPU	EX5B_BORBU	YOR1_CALSR	YGP1_YEAST	SACB_ERWAM	
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ALIGNMENTS

TENGLY T. CTNB_HUMAN STANDARD; PRT; 781 AA. AC P35522 AC P355224 DT O1-FEB-1994 (Rel. 28, Last sequence update) DT O1-FEB-1994 (Rel. 28, Last sequence update) DT O1-FEB-1994 (Rel. 28, Last sequence update) DT O1-MAR-2002 (Rel. 41, Last annotation update) DT O1-MAR-2002 (Rel. 41, Last annotation update) DT O1-MAR-2002 (Rel. 41, Last annotation update) CTNNB1 OR CTNNB. CTNNB1 OR CTNNB. OC Beta-catenin. Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. OX NCB1_TAXID=9606; RX NCB1_TAXID=95105247; PubWed=7806582; RX MEDLINE=95105247; PubWed=7806582; RX MEDLINE=95105247; PubWed=7806582; RX MEDLINE=95105247; PubWed=7806582; RX MEDLINE=95105247; PubWed=10679188; RY FRY RR MEDLINE=20014941. RY MEDLINE=20014941; PubWed=10679188; RY MEDLINE=20078806; PubWed=1113674; RY MEDLINE=20078806; PubWed=1113674; RY MEDLINE=20078806; PubWed=1113674; RY MEDLINE=20078806; PubWed=1113674; RY MEDLINE=20078806; PubWed=1113074; RY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 13.2.461. RY MEDLINE=20078806; PubWed=1113074; RY MEDLINE=200780606; RY ME	a c c c c c c c c c c c c c c c c c c c
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TARGET CALL DESCRIPTION OF CELL ADHESION AND IN MOTIVE CALL MOTIVE CALL DESCRIPTION OF CELL ADHESION AND IN THE CHUCTION: INVOLVED IN THE NUT PATHWAY.

CONTRACT TRANSDIOUTION THROUGH THE WAT PATHWAY.

CONTRACT THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND CONTRACTS WITH APC AND CONTRACTS WITH APC AND CONTRACTS WITH APC AND CONTRACTS AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND CONTRACTS WITH ALCHARACATENIN AND CONTRACTS WITH ALCHARACATE ON THE CADHERIN COMPLEX WITH CONFICENT WITH ALCHARACATE ON THE NUCLEUS WHEN IT IS UNSTABILIZED (LOW LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS STABILIZED (LOW LEVEL OF PHOSPHORYLATION).

CONTRACT OF THE ACTION OF GSK-3B. WNT-DEPENDENT ACTIVATION CONTRACTIVATION OF RESULTING IN ITS ACCUMULATION IN CYTOPLASM.
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                 Pokutta S., Weis W.I.; "Structure of the dimerization and beta-catenin-binding region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSTIE; PS50176; ARM REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D708F170A3FBED6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                        -i SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
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100.0%; Pred. No. 7.5e-22;
ative 0; Mismatches 0;
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ARM 7.
ARM 8.
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PDB; 2BCT: 15-0CT-97.
PDB; 3BCT: 19-NOV-97.
PDB; 1DCW: 12-JUL-00.
TRANSFAC; T02984; -.
MGD; MGI: 88276; Catnb.
Pfam; PPF00514; Armadillo.
Pfam; PRO0514; Armadillo.seg; 12.
SMART; SM00185; ARM; 11.
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              MEDLINE-20337986; "PubMed-10882138;
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Best Local Similarity 100.
Matches! 43; Conservative
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                                                                     alpha-catenin.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"Three-dimensional structure of the armadillo repeat region of beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                   protein; Nuclear protein;
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Butz S., Stappert J., Weissig H., Kemler R.;
"Plakoglobin and beta-catenin: distinct but closely related.";
Science 257:1142-1144(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Regulation of beta-catenin signaling in the Wnt pathway.";
Blochem. Blophys. Res. Commun. 268:243-248(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB78F165A3EEF86E CRC64;
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MEDLINE=97442350; PubMed=9298899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 212; DB 1;
1larity 100.0%; Pred. No. 7.5e-22;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 AA
                                                                                                                                                   InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; II.
PR051TE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural 1
                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20145417; Pubmed-10679188;
                                                                                                                                                                                                                                                                     ARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85496 MW;
                                                EMBL; X87838; CAA61107.1; -
EMBL; Z19054; CAA79497.1; -
PIR; S31988; S31988.
PDB; 1G3J; 17-JAN-01.
TRANSFAC; T02872; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sell 90:871-882(1997).
                                                                                                                                                                                                                                                  Repeat; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTNNB1 OR CATNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-catenin.
                                                                                                                                          MIM; 116806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ikuchi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTNB_MOUSE
Q02248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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CTNB_MOUSE RESULT

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Gaps

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43

Length 781; Indels . :

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                                                                                                                                                                                                                                                                                                                                                                                                                                    C SIMILARITY).
C -1- SUBCELLULAR LOCATION: CYTOPLASMIC WHEN IT IS UNSTABILIZED (HIGH
C LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS
C LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS
C -1- TISSUE SPECIFICITY: EXPRESSED IN THE TESTIS.
C -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED AT E30-60 DAY DPC.
TESTIS. REDUCED EXPRESSION AT E90 DAY DPC.
C -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B. WHY-DEPENDENT ACTIVATION
C -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B. PHOSPHORYLATION OF BETA-
C GATENIN IS REDUCED AND THE PROTEIN IS NO LONGER DEGRADED,
CC ATENIN IN TESTICAL DAY OF CATENIN FAMILY.
CC -1- SIMILARITY: CONTAINS 12 ARM REPEATS.
CC -1- SIMILARITY: CONTAINS 12 ARM REPEATS.
CC -1- SIMILARITY: CONTAINS 12 ARM REPEATS.
                                                                                                                                                                                                                                                                            J. Cell. Physiol. 181:258-272(1999).

-!- FUNCTION: INVOLED IN THE REGULATION OF CELL ADHESION AND IN SIGNAL TRANSDUCTION THROUGH THE WIT PATHWAX (BY SIMILARITY).

-!- SUBUNIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND E-CADHERIN. THE NUCLEAR FORM BINDS TCF/LEF. I AND MAY ALSO BIND PONTINS AND DUFLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CACHERIN COMPLEX TO THE CORTICAL ACTIN CYTOSKELETON (BY
                                                                                                                                                                                                            MEDLINE=99428593; PubMed=10497305;
Chung S.S.W., Lee W.M., Cheng C.Y.;
"Study on the formation of specialized inter-Sertoli cell junctions in
                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9C29186B6DD54B87 CRC64;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
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SMART; SM00185; ARM; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF121265; AAD28504.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85454 MW;
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637
781 AA;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-catenin
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                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                         Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                         MEDLINE=92073903; PubMed=1962194;
McCrea P.D., Turck C.W., Gumbiner B.M.;
"A homolog of the armadillo protein in Drosophila (plakoglobin)
assoclated with E-cacherin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3ECD27232239F799 CRC64;
307 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%; Score 208; DB 1; 97.7%; Pred. No. 2.7e-21;
                                                                                                         01-MAY-1992 (Rel. 22, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                      781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                             Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARM 1.
ARM 2.
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ARM 4.
ARM 5.
ARM 7.
ARM 7.
ARM 9.
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SMART; SM00185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; $35099; $35099.
HSSP; 00248; 2BCT.
TRANSFAC; 1703026; Armadillo.
InterPro; IPR000225; Armadillo.
                                                                                           01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M77013; AAA49670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 97.7
Matches 42; Conservative
                                                                    STANDARD;
                                                                                                                                                                                  Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 AA;
                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                  Beta-catenin.
                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                  Xenopodinae;
                                                                      CTNB_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query! Match
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                                                        CTNB_XENLA
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43

1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV

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Gaps

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Length 781; Indels

100.0%; Score 212; DB 1; 100.0%; Pred. No. 7.5e-22; ive 0; Mismatches 0;

43; Conservative

Best Local Similarity Matches 43; Conserv

Query Match

307 GNQESKLIILASGGPQALVNIMRTYSYEKLLWTTSRVLKVLSV 349

Q

820 AA

STANDARD;

CTNB_TRIGR

CTNB_TRIGR RESULT

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                                                                                                                                                                                                                 "Identification of homologues to beta-catenin/plakoglobin/armadillo in two invertebrates, Urechis caupo and Tripneustes gratilla."; Biochim. AND PERHAPS TO CHER (MEMBRANE) PROTEINS. THE ASSOCIATION OF CAPTENINS TO CAPHERINS PRODUCES A COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                               Eukaryota; Mětazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NW 8.
NW 9.
NW 10.
57255E0F57795FD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 GNQESKLIILASGGPAALVHIMRTYDYEKLLMTTSRVLKVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
                       (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                     Tripneustes gratilla (Hawaian sea urchin).
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ARM 1.
ARM 2.
ARM 4.
ARM 5.
ARM 6.
ARM 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 12.
PROSITE; PS50176; ARM_REPEAT; 9.
                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-93305730; Pubmed-8318544; Rosenthal E.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q02248; 1DOW.
InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.0%;
ilarity 93.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L10354; AAA30089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S33794; S33794.
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Best Local Similarity
Matches 40; Conserv
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283
367
406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644
820 /
                                                                                                                                              NCBI_TaxID=7673;
                                                                                                                                                                                                                                                                                                                                              PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell adhesion
                                                                       Beta-catenin.
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PLAK_HUMAN
ID PLAK_HUMAN
                                                       01-MAR-2002
                                                                                                                                   Tripneustes.
                          01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
SEQUENCE
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REPEAT
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Interproj IPR000225; Armadillo.
Pfam: PF00514; Armadillo_seg; 10.
SMARY: SM00185; ARM; 8.
PROSITE; PS0176; ARW, REPEAT; 8.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.

EMBL; M23410; AAA64895.1; -. PIR; A32905; A32905.

HSSP; Q02248; 2BCT. MIM; 173325;

PROBABLE

Cell adhesion; INIT_MET C

REFEAT REPEAT REPEAT

ARM

-i- SUBUNIT: HOMODIMER.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-

-i. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.

ASSOCIATED FORM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (Human)

JUP OR DP3

NCBI_TaxID=9606;

Ol:APR-1990 (Rel. 14, Last sequence update) 01:WAR-2002 (Rel. 41; Last annotation update) Junction plakoglobin (Desmoplakin III).

018APR-1990 (Rel. 14, Created)

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ARM 8.

GQLA -> DSSL (IN REF. 1; AAA64895).

V -> A (IN REF. 1; AAA64895).

472741F400D388FD CRC64;
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Pred. No. 2.4e-19;
2; Mismatches 2;
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Best Local Similarity '90.7%;
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PLAK_MOUSE RESULT

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                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                          -i- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMBRIS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOGLOBIN IN BOTH THE DESNOSOMES AND IN THE
INTERNEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
ASSOCIATED FORM.
                                                                                                                                                MEDLINE-92376536; PubMed-1509266; Butz 8., Stappert J., Weissig H., Kemler R.; Plakoglobin and beta-catenin: distinct but closely related."; Science 257:1142-1142-1144(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
                                                                                                                                                                                                                    Butz S.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17CF444607422BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS AT LEAST 9 ARM REPEATS.
                                 01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III) (Fragment).
  621 AA
  PRT;
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ARM
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SMART; SM00185; ARM; 8.
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InterPro; IPR000225; Armadillo.
                       Created)
                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M90365; AAB02885.1; -. PIR; S35092; S35092.
                                                                                                                                                                                                        REVISIONS TO 294 AND 296.
 STANDARD;
                                                                             Mus musculus (Mouse)
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                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=10090;
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                      01-JUL-1993
PLAK_MOUSE
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-i. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.

MEDLINE-93305730; PubMed-8318544;

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NCBI_TaxID=6431; SEQUENCE FROM N. Rosenthal E.T.;

01-FEB-1994 (Rel.:28, Created) 01-FEB-1994 (Rel.:28, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)

818 AA

STANDARD;

ÜRECA

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Musca domestica (House fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                     Gaps
                     ö
                    Indels
                                       3
Score 190; DB 1;
Pred. No. 9.6e-19;
                                                                                                                                              , Last sequence update)
                                                                                                                 813 AA
                    1; Mismatches
                                                                                                                                                                 Armadillo segment polarity protein.
                                                                                                                                    01 -JUL-1993 (Rel. 26, Created)
89.68;
                     Conservative
                                                                                                                :STANDARD;
        Best Local Similarity
Matchès ½ 39; Conserv
                                                                                                                                                (Rel.
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                                                                                                                                              01-JUL-1993
01-MAR-2002
                                                                                                                ARM_MUSDO
002453;
Query: Match
Best Local 8
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3; Indels

2; Mismatches

Conservative

Best Local Similarity Matches 38; Conser

Query Match

1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 43

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89.6%; Score 190; DB 1; Length 621; 88.4%; Pred. No. 7e-19;

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Length 818;

1DF174BEEF745C1D CRC64;

89070 MW;

REPEAR SEQUENCE

protein; Repeat.

Structural

Cytoskeleton;

Cell adhesion;

InterPro; IPR000225; Armadillo. Pfan; PF00144; Armadillo_seg; 12. SMAR; SM0185; ARW. 11. PROSITE; PS50176; ARM_REPEAT; 9.

EMBL; L10355; AAA30330.1; -.

HSSP; (002248;

ARM 1.
ARM 2.
ARM 3.
ARM 4.
ARM 5.

REPEAT REPEAT REPEAT REPEAT

REPEAT

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REMEDLINE-20196006; Pubbed-10/31122;

RA Admandides PG., Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.,

RA Admandides PG., Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.,

RA Admandides PG., Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.,

RA Admandides PG., Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.,

RA GUTCO, G.G., Wortnand J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brindon R.C., Rogers Y. H.C., Blazej R.G., Change M., Pichiffer B.D.,

RA Abril'J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M. Basu A. Baxendall J., Bayrakaroglu L., Basaley E.M.,

RA Besson K.Y. Bence P.V., Berman B.D., Bhandari D., Bolshakov S.,

RA Beritis K.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Duny L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Hostin D., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,

RA Hostin D., Houston K.A., Hewland T.J., Well M.-H., Ibeywam C.,

A Lasko, P., Lei Y., Levitsky A.A., Li J., MIND, D., Lai Z.,

RA Lasko, P., Lei Y., Levitsky A.A., Li J., Li J., Lin X.,

RA Lasko, P., Lei Y., Levitsky A.A., Li J., Li J., Lin X.,

RA Lasko, P., Lei Y., Levitsky A.A., Li J., Li J., MIND, W. Moshrefi A.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Bazzolo M., Pittman G.S., Pan S., Pollard J., Putl V., Reese M.G.,

RA Shie B.C., Siden Kiamos I. Singson M., Strong R., Such B.,

RA Shie B.C., Starbing R., Shon M., Strong R., Shon H.,

RA Shie B.C., Starbing M., Weinstock G.M., Weissenbach J.,

RA Shie B.C., Starbing M., Zhong W., Zhon Y., Zhu X., Smith H.O.,

RA Shie B.C., Starbing M., Shon S., Zhan M., Zhong G., Zhu X., Smith H. Shon S., Zhan M., Woodger T., Wolley W., Zhu W., Zhong S., Zhu X., Zhu X., Zhu X., Smith H. Shon S.,

Ra Sheng X.H., Zhong F.N.,
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                                                        Riggleman B., Wieschaus E., Schedl P., "Molecular analysis of the armadillo locus: uniformly distributed withing riper and a sprotein with novel internal repeats are associated withing Drosophila segment polarity gene."; Genes Dev. 3:96-113(1989).
                                                                                                                                                                                                            SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                        Loureiro J., Peifer.M.; Roles of Armadillo, a Drosophila catenin, during central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
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                                                   MEDLINE-89211895; PubMed-2707602;
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                                                                                                                                                                                                                                                                                                                                                                      development
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                                 STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                          TISSUE-Head; ..
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Brosophia melanogacier (Fruit fly).
Brukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                               housefly Musca domestica.";
J. Mol. Evol. 36:224-233(1993).
-!- FUNCTION: SEGMENT POLARITY PROTEIN. MUTATION IN ARM PRIMARILY
AFFECT THE POSTERIOR PAT OF THE SEGMENT AND LEAD TO THE
PRODUCTION OF ANTER.OR STRUCTURES WITHIN THIS REGION. MAY BIND
A CADHERIN AND PARTICIPATE IN THE TRANSMISSION OF DEVELOPMENTAL.
                                                                                                                                          Pelfer M.A., Wieschaus E.; "The product of the Drosophila melanogaster segment polarity gene armadillo is highly conserved in sequence and expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: INNER SURFACE OF CELL MEMBRANE. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 10 ARM REPEATS.
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73E61F59BDBFA580 CRC64;
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ASP/GLU-RICH (ACIDIC).
ARM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
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Pfam; PF00514; Armadillo_seg; 12.
SMART; SM0185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Struct
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MEDLINE-93247062; PubMed-8483160;
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            Muscoidea; Muscidae; Musca.
NCBI_TaxID=7370;
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION.
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1. SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED WITH THE CNS AND EPIDERMIS.

1. SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED WITH THE INNER SUFFACE OF CELL MEMBRANE.

1. SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED WITH THE SUFFACE OF CELL MEMBRANE.

1. SUBCELLULAR LOCATION: CYTOPLASMIC SPLORM IS PREDOMINANT BEFORE GERM BADD RETRACTION, AFTER RETRACTION AND DURING LARVAL STAGES, IT IS FOUND IN HIGH LEVELS IN SPECIFIC CELLS ALONG THE CNS MIDLINE.

2. TISSUE SPECIFICITY: CYTOPLASMIC ISOFORM IS PREDOMINANT BEFORE GERM BAND RETRACTION IN THE CNS MIDLINE.

3. SOFORMS ATTER SEEN AFTER GERM BAND RETRACTION IN THE CNS MIDLINE.

4. TISSUE SECRIFICATE OF THE CNS, ALSO PRESENT IN AXONS DURING LARVAL STAGES

AND ACCUMULATES IN THE PNS.

5. SOFORMS AND ACCUMULATES IN THE PNS.

5. HIGHEST LEVELS DURING EARLY TO MID-EMBRYOGENESIS.

6. HIGHEST LEVELS DURING EARLY TO MID-EMBRYOGENESIS.

7. PTM: PHOSPHORYLATED ON SER, THR AND TYR RESIDUES. LEVEL OF FROM PARLES BOTH DURING EMBRYONIC DURING MEMBRY AND FROM PARLES BOTH DURING EMBRYONIC DURING MEMBRY AND PROPERMY AND SERVER THE POSTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                    Peifer M., Pai L.-M., Casey M.;
"Phosphorylation of the Drosophila adherens junction protein Armadillo: roles for wingless signal and zeste-white 3 kinase.";
Dev. Biol. 166:543-556(1944).
-: FUNCTION: NEURAL ISOFORM MAY ASSOCIATE WITH CADN AND PARTICIPATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBRYONIC TISSUE TO TISSUE. SGG IS REQUIRED FOR PHOSPHORYLATION AND WG SIGNAL MEGATIVELY REGULATES ARM PHOSPHORYLATION.
HYPOPHOSPHORYLATED FORM OF ARM INCREASES IN STRADY-STATE LEVELS.
SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
SIMILARITY: CONTAINS 12.5 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50176; ARM_REPEAT; 9.
Developmental protein; Segmentation polarity protein; Repeat;
Cell adhesion; Cytoskeleton; Structural protein; Phosphorylation;
Alternative splicing.
  sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASP/GLU-RICH (ACIDIC).
ARM 1.
ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: AF001213; AAB58731.1; --
EMBL: AE0012213; AAB56881; ALT_INIT.
EMBL: AL021106; CAA15946.1; --
EMBL: AL021086; CAA15946.1; JOINED.
EMBL: AL021086; CAA15935.1; --
EMBL: AL021106; CAA15935.1; --
EMBL: AL021106; CAA15935.1; JOINED.
                                                                                                                MEDLINE=95113174; PubMed=7529201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0000117; arm.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2220-2222(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X54468; CAA38350.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85; ARM; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
326
368
410
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REPEAT
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RANGE STANDARD BANGARANA BANGA STANDA STANDA
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                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93093332; PubMed-1459359; Franke W.W.; Franke W.W.; Sulpalmann R., Franke W.W.; Identification of plakcglobin in occytes and early embryos of Renopus laevis: maternal expression of a gene encoding a junctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de Marais A.A., Moon R.T.; "The armadillo.homologs beta-catenin and plakoglobin are differentially expressed during early development of Xenopus
                                                                                                                                                                                                                                                                                                     Ouery March 87.7%; Score 186; DB 1; Length 843; Best Local Similarity, 88.4%; Pred. No. 3.6e-18; Matches 38; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 315 GNQESKLIILASGGPNELVRIMRSYDYEKLLWTTSRVLKVLSV 357
                                                                                                                                                                                                                                                                                                                                                                                           43
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                                                                                                                                                                                                                                                                                                                                                                             412 ) GNOESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707579
01-70L-1993 (Rel. 26, Last sequence update)
01-70L-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III).
    ARM 8.
ARM 9.
ARM 10.
ARM 11.
ARM 12.
ARM 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 133-292 FROM N.A. MEDLINE=93012479; PubMed=1397690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Differentiation 51:187-194(1992)
                                                                                                                                                                                                                                             91152 MW;
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                                                                                                           689
843
843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATED FORM
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                                                                 585
609
648
690
718
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                                                                                                                                                      VAŘŠPLIC
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REPEAT
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                                                                 REPEAT
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TISSUE-Liver;
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018920;
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CARBOHYD
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SEQUENCE
                                      CARBOHYD
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0
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Mandriota S.J., Pepper M.S.;

Megulation of angiopotetin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia.";

endothelial cells by cytokines and hypoxia.";

Circ. Res. 83:852-859(1998).

-1-FUNCTION: BINDS AND ACTIVATES TIES RECEPTOR BY INDUCING ITS TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD VESSEL MATURATION/STABLLITY. IT MAY PLAY AN IMPORTANT ROLE IN THE HEART EARLY DEVELOPMENT.

-1-SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                       Length 738;
                                                                                                                                                                                                                                                                                             Indels
                                                                                               Structural protein; Repeat.
                                                                                                                                                                                                                  -> V (IN REF. 2).
-> T (IN REF. 2).
569DBE69D08BBC58 CRC64;
                                                                                                                                                                                                                                                                                                                             294 GNQESKLIILGNGGPQGLVQIMRNYNYEKLLWTTSRVLKVLSV 336
                                                                                                                                                                                                                                                                                                                  1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 43
                                                                                                                                                                                                                                                               Score 185; DB 1; Le
Pred. No. 4.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            110 AA
                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Placenta;
                                                                                                         ARM 1.
ARM 2.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 9.
ARM 90.
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiopoietin-1 (ANG-1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98451564; PubMed=9776732;
                                                   Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; ID.
PR051TE; P550176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Stru
                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF030376; AAC78246.1; -.
                                                                                                                                                                                                                                         81711 MW;
 EMBL; X67078; CAA47463.1; -. PIR; S24636; S24636. PIR; S35093; S35093.
                                                                                                                                                                                                                                                                         87.3%;
86.0%;
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                      251
293
377
416
460
506
547
609
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                          738 AA;
                                         Q02248; 2BCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                              AGP1_RAT
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                CONFLICT
                                                                                                                               REPEAT
REPEAT
REPEAT
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"Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia.";
"Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia.";
circ. Res. 83:852-85(1998).
-!- FUNCTION: BINDS AND ACTIVATES TIEZ RECEPTOR BY INDUCING ITS
-!- FUNCTION: BINDS AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A PROCESSES LATER AND DISTINCR RECIPENCAL INTERACTIONS BETWEEN THE SUDDITIONS BETWEEN THE STUDY STATEMENT OF VESSEL MATURATION STABLISTY. IT MAY PLAY AN IMPORTANT ROLE IN THE HEART EARLY DEVELOPMENT (BY SIMILARITY).
-!- SUBCRELLUTAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Cvary; ...
MEDILINE-99054348; PubMed-9840613;
MEDILINE-99054348; FubMed-9840613;
Goede-V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
"Analysis of blood vessel maturation processes during cyclic ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine)...
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                           Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                 110 AA; 12860 MW; 36D345DECB1E1845 CRC64;
                                                                                                                    COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2 NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64. NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update) Angiopoietin-1 precursor (ANG-1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                 Score 54.5; DB
Pred. No. 0.94;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 AA
Interpro: IPR002181; Fibrinogen_C.
Glycoprotein; Coiled coil.
NOWYTER 63 109. COILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98451564; PubMed-9776732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lab. Invest. 78:1385-1394(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF093573; AAC61872.1; -. EMBL, AF032923; AAC78245.1; -. HSSP; P02671; 1F2D.
                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.7%;
Best Local Similarity 42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 91-200 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches , 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                    109.
32.
64.
110.
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Best Local Similarity 42.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                        1119
261
122
122
154
265
265
   -1- PTM: GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                 498 AA;
                                            : : ISCHEMIC HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_TaxID=10090;
                                                                                                                                                                                                                                                                                          81
153
284
1122
1152
293
293
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CARBOHYD
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008538;
                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                               DOMAIN
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   δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Fetal lung;
MEDLINE=97134663; PubMed=8980223;
Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 1:77-35(1994).

-1- FUNCTION: BINDS AND ACTIVATES TIEZ RECEPTOR BY INDUCING ITS TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A CRCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE HEART EARLY DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Bone marrow;
MEDLINE=96051387; PubMed=7584026;
Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                       (POTENTIAL).
                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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"Isolation of anglopoletin-1, a ligand for the TIE2 receptor,
secretion-trap expression cloning.";
Cell 87:1161-1169(1996).
                                                                                                                                                                                                 Score 54.5; DB 1; Length 481;
Pred. No. 5.3;
5; Mismatches 11; Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohara O., Nagase T., Kikuno R., Nomura N.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  BEEC9ED84FC2BB50 CRC64;
                                                               ANGIOPOIETIN-1.
COILED COIL (POTENTIAL).
FIBRINGEN C-TERMINAL.
                                                                                                                                                                                                                                                           154 NQTSRLEI-----QLLENSLSTYKLEKQLLQQTNEILKI 187
                                                                                                                                                                                                                                               NQESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                          498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL
                             PROSITE; PS00514; FIBRIN AG_C_DOMAIN; 1. Glycoprotein; Coiled coil; Signal.
                                                      POTENTIAL
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InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
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ANGPT1 OR KIAA0003.
                                                                                                                                                                  55556 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 307-498 FROM N.A.
                                                                                                                                                                                                 Query Match 25.7%;
Best Local Similarity 42.5%;
Matches 17; Conservative
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>481
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                  481 AA;
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153
283
283
92
122
154
154
481
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Q15389;
                                                                                                CARBOHYD
CARBOHYD
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SEQUENCE
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CARBOHYD
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DOMAIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use; by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or,send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>``</u>
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
-1'-MISCELLANEOUS: IT-MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE IF CAN BE USED FOR;SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR FEPROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97134663; Pubwed-8980223;
Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DUE TO
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N-LINKED (GLONAC. .) (POTENTIAL).
M-LINKED (GLONAC. .) (POTENTIAL).
MISSING (IN CELL LINE T98G; MAY BE DU
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7:
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Pred. No. 5.5;
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                                                                                                                                  F. SIMILARITY: CONTAINS 1 FIBRINGGEN C-TERMINAL DOMAIN.
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5D5FA63AEF6BE920 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR002181; Fibrinogen_C.
Pfam: PF00147; fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Glycoprotein; Coiled coil; Signal; Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NOESKLIILASGGPQALVNIMRTYTYEK-LLWTTSRVLKV 40
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16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U83508; AAB50557.1; -.
EMBL; D13628; BAA02793.2; ALT_INIT.
HSSP; P02671; 1FZD.
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(M.20) 4 8-1 - (M.20) 41 Search completed: July 29, 2002, 16:09:53 Job time: 758 sec

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Gaps

7;

Query Match 25.7%; Score 54.5; DB 1; Length 498; Best Local Similarity 42.5%; Pred. No. 5.5; Matches 17; Conservative 5; Mismatches 11; Indels

<u>:</u>:

. . .

Compugen Ltd. GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

- protein search, using sw model OM protein

July 29, 2002, 16:12:04; Search time 124.4 Seconds (without alignments) 59.797 Million cell updates/sec Run on:

1 GNQESKLIILASGGPQALVN.....TYTYEKLLWTTSRVLKVLSV US-09-641-104A-8 212 Title: Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 Total number of hits satisfying chosen parameters:

562222 seqs, 172994929 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

splant:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_human:* sp_invertebrate:* sp_mammal:* sp_rvirus:* sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_organelle:* sp_phage:* sb_mhc:* 111: 123: 144: 115: 116: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

			Description		Q90424 brachydanio	09d335 mus musculu	042486 gallus gall	P79321 sus scrofa	Ogovf7 brachydanio	061229 lytechinus	015151 homo sapien	O9bwc4 homo sapien	P70565 rattus norv	Ogn144 ciona intes	076152 ciona savid	025100 hydra magni	018825 caenorhabdi	044326 caenorhabdi	O9vdw9 aeropyrum p	Ogoges a compress s
CHILINA			ID		090424	Q9D335	042486	P79321	O9PVF7	061229	015151	O9BWC4	P70565	Q9NL44	076152	Q25100	018825	044326	6MQX6O	Q9P8C8
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ALIGNMENTS

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SEQUENCE FROM N.A..

MEDLINE=96122902; PubMed=8562427;

MEDLINE=96122902; PubMed=8562427;

Melly,G.M., Erezylinaz D.F., Moon R.T.;

"Induction of a secondary embryonic axis in zebrafish occurs following the overexpression of beta-catenin.";

Mech. Dev. 53:261-273(1995).

EMBL: U41081; AAC59732.1;
                                                                                                                                                    Brachydanio rerio (Zebrafish) (Zebra danio).

Brachydanio rerio (Zebrafish) (Zebra danio).

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 212; DB 13; Length 780; Best Local Similarity 100.0%; Pred. No. 3.9e-21; Matches 43; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D7A1FB80F94066DC CRC64;
                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                          780 AA
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                 HSSP; P5522; 1G37.
ZFIN; ZDB-GENE-980526-362; ctnnb.
Interpro; IPR000225; Armadillo.
Pfan; PP00514; Armadillo.seg; 12.
SMART; SMO0185; ARM; 11.
PROSITE; PSS0176; ARM_REPEAT; 8.
SEQUENCE 780 AA; 85542 MW; D7A1
                                          PRELIMINARY;
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CTNNB.
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RESULT : 1
090424
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Gaps

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Indels

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349 43

Length 781;

090335

RESULT Q9D335

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Winteroe A.K., Fredholm M., \mbox{\tt "Evaluation} and characterization of a porcine small intestine cDNA \mbox{\tt "Evaluation}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                  Lisolation and characterization of chicken beta-catenin."; Gene 196:201-207(1997).
EMBL; U82964, AAB80856.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. EMBL; 284131; CAB06327.1; ...
HSSP; P35222; 1633.
InterPro: JPR000225; Armadillo.
Pfan; PF00514; Armadillo_seg; 2.
PROSITE; PS50176; ARM_REPEAT; 2.
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6D205D9A4DBAC562 CRC64;
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(TremBirel. 13, Last sequence update)
(TremBirel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33, GNOESNLIILASGGPQALVNIMRTYTYEKLLMTTSRVLKVLSV
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Pred. No. 3.9e-21;
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Pred. No. 2.4e-21;
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SEQUENCE FROM N.A..
STRAIN-WHITE LEGHORN: TISSUE-DORSAL SKIN;
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                            Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
                                     MEDLINE-97464068; PubMed-9322759
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                                                                                                                                                                          PROSITE, PS50176; ARM_REPEAT; SEQUENCE 781 AA; 85438 MW;
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Best Local Similarity 100.0%;
Matches 43; Conservative 0
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97.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA CATENIN (FRAGMENT).
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01-MAY-2000 (
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                P79321;
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                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE COLON CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:9030417H18, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARM_REPEAT; 7. 85546 MW; 937538C3B5CD75D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GNOESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 43
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Last annotation update)
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                                                       781 AA
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                                                       PRT;
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InterPro; PPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART: SM00185; ARM; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
EMBL; AK018515; BAB31250.1; -.
HSSP; P35222; 1G3J.
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042486;
01-JAN-1998 (TrEMBLrel. 05,
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                                                       PRELIMINARY;
                                                                                                                                                                                Mus musculus (Mouse).
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                                                                                                                                                                                                                                                         FROM N.A.
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Gaps

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Indels

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Length 117;

Euteleostomi;

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Ozawa'M., Nuruki K., Toyoyama H., Ohi Y.; "Cloning of an alternative form of plakoglobin (gamma-catenin) lacking
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89264555; pubmed-2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
Schiller D.L., Cowkin P.,
"Molecular cloning and amino acid sequence of human plakoglobin, the
common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11016852;
Whittock N.V., Eady R.A.J., McGrath J.A.;
"Genomic Organization and amplification of the human plakoglobin
                                                                                                                    Homó sapiens (Human).
Eŭkaryota, Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NOBILTAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
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745 AA; 81744 MW; 3519A0973748BCF4 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DDC-2001 (TrEMBLrel. 19, Last annotation update)
JUNCTION PLAKOGLOBIN.
                                Last sequence update)
Last annotation update)
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EMBL; AF233882; AAG16727.1; JOINED.
HSSP; Q02248; ZBCT.
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MEDLINE-96157724; PubMed-8576101;
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Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene ";
Expt. permatol. 9:323-326(2000).
EMBL: Z68228; CAA92522.1; -.
EMBL: D50808; BAA09435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the fourth armadillo repeat.";
J. Biochem. 118:836-840(1995).
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  01-NOV-1996 (TrEMBLrel. 01, 01:NOV-1996 (TrEMBLrel: 01, 01:01) 01:JUN-2001 (TrEMBLrel: 17, PI, NOV-101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                 SEQUENCE FROM N.A.

IX MEDLINE-99386700; PubMed=10456847;
Carda J., Reidenbach S., Pratzel S., Franke W.W.;
Carda J., Reidenbach S., Pratzel S., Franke W.W.;
Carda J., Reidenbach S., Pratzel S., Franke W.W.;
T. "Cadherin-catenin complexes during zebrafish oogenesis: heterotypic
T. "Cadherin-catenin complexes and follicle cells.";
Biol. Reprod. 51:692-704(1999).
Biol. Reprod. 51:692-704(1999).
RESP: Q02248: IDDOW.
RESP: Q02248: IDDOW.
RESP: Q02248: IDDOW.
REPPOS. INFO00225; Armadillo.
REPPOS. TROMO185; Armadillo.
REPOS. RESP: SARM. REPEAT; 8.
RESS: RESS: RAW. REPEAT; 8.
RESS: RESS: RAW. REPEAT; 8.
RESE: RESS: RAW. REPEAT; 8.
RESE: RESS: RAW. REPEAT; 8.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
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Pred. No. 1e-18;
1; Mismatches 2; Indels
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SWART: SW00185; ARW; 12.
PROSITE; PS00687; ALDEHYDE_DEHYDE_GLU; UNKNOWN_1.
SEQUENCE 821 AA; 89558 WW; 71E21D562A99CSAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 GNQESKLIILANGGPEGLVNIMRTYNYEKLLWTTSRVLKVLSV 329
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA CATENIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%; Score 197; DB 13; 90.7%; Pred. No. 4.6e-19; live 2; Mismatches 2;
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InterPro; IPR000225; Armadillo.
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Best Local Similarity 93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Conservative
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona.
                                                                  Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona. ;
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MEDLINE=98443204; PubMed=9769178;

MEDLINE=98443204; PubMed=9769178;

Yeshida S., Marikawa Y., Satoh N.;

Yeshida S., Marikawa Y., Satoh N.;

Regulation of the trunk-tail patterning in the ascidian embryo: a possible interaction of cascades between lithium/beta-catenin and localized maternal factor pem.";

Dev. Biol. 202:264-279(1998).

EMBL: AB012160; BAA327891; -.

HSSP; P35222; 1G33.
                                                                                                                                                                                                             Imai K., Takada N., Satoh N., Satou Y.;
"An essential role of beta-catenin in the endoderm specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                               ascidian embryo.";
Submitted (AUG-1199):to the EMBL/GenBank/DDBJ databases.
EMBL;:ABO11543; BAA92185.1; -.
HSSP; P35222; 1G3J.
                                                                                                                                                                                                                                                                                                                                                           InterPro; 1PR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM0185; ARM; 11.
SEQUENCE: PS50176; ARM REPEAT; 6.
SEQUENCE: 769 AA; 84703 MW; F61CC489B436E1BC CRC64;
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Last annotation update)
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:88.4%; Pred. No. 1.3e-17;
ative 1; Mismatches 4;
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Best Local Similarity 88.4%; Pred. No. 1.2e-17;
Matches 38; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            806 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00
025100 PRELIMINARY; PRT;
025103;
01-NOV-1996 (TEMBLREL 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; 9.
PROSITE; PS050176; ARM_REPEAT; 7.
SEQUENCE 773 AA; 85217 MW; C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query.Match :- .88.2'
Best Local Similarity :88.4'
Matches : 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                 Clona intestinalis.
                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                  NCBI_TaxID=7719;
BETA-CATENIN.
CIBETA-CATENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA-CATENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT: 12
Q25100 .
ID Q25100
AC Q25100
DT 01-NOV-
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     DDE RELEASE DE SO 
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Eukaryota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Umekita Y., Liao S.; "Molecular cloning and sequencing of the rat plakoglobin cDNA."; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U58889; AAB06317.1; --
HSSP; Q02248; 2BCT.
        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                               Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC000441; AAH00441.1; -.
EMBL; BC011865; AAH11865.1; -.
                                                                                                                                                                                                             HSSP; 002248; 2BCT.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARW, 12.
PROSITE; PS50176; ARW_REPEAT; 7.
SEQUENCE 745 AA; 81726 MW; 34DF7BFB4748BCF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                District of PR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM0185; ARM; 8.
BROSITE; P550176; ARM_REPEAT; 7.
SEQUENCE 745 AA; 81777 MW; 9E2F52910A7ACD41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 GNQESKLIILANGGPQGLVQIMRNYSYEKLLMTTSRVLKVLSV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 GNQESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVLSV 340
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.5%; Score 194; DB 4; I
Best Local Similarity 90.7%; Pred. No. 1.3e-18;
Matches 39; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 190; DB 11;
Pred. No. 4.6e-18;
2; Mismatches 3;
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STRAIN-SPRAGUE-DAWLEY; TISSUE-VAGINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-VAGINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                       SEQUENCE FROM N.A.
TISSUE-PLACENTA, CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.6%;
88.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.4
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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P70565;
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EMBL; AF0108653; AAB94552.1; -.
EMBL; 281564; CAB04572.1; -.
HSSP; P35222; 1G3J.
           (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
STRAIRML BRISTOL;
COSTA M., Raich W., Agbunag C., Hardin J., Priess J.R.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74510 MW; E6C7ED51F6241232 CRC64;
                                                                                                                                                                                        97D6FFDE71BDFDFF CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 38.4 KDA PROTEIN APE0800.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 NTEQKIKFVKMGGPQKLLMLLQHRVYENLLWRTTQLLKTFS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLS 42
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                                                                                                                                                                                                                                                                                          Ouery Match 42.9%; Score 91; DB 5;
Best Local Similarity 41.5%; Pred. No. 0.0004;
Matches 17; Conservative 9; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 AA.
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Pfam; PF00514; Armadillo_seg; 6.
PROSITE; PS50176; ARM_REPEAT; 1.
                                                                                                                                                  A: 92227 MW;
                                         EMBL; U46673; ÅAC48154.1; -.
EMBL; AF063646; AAC17424.1;
HSSP; Q02248; 3BCT.
TRANSFAC; T03880; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                        811.AA;
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           Submitted
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SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

SEQUENCE—94150718; PubMed=7906398; Replain of the property of the 
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                              Hydra magnipapillata (Hydra).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
NCBI_TaxID=6085;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-WILDTYPE 105;
MEDLINE-96257271; PubMed-8654977;
Hobmayer E., Hatta M., Fischer R., Pujisawa T., Holstein T.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.1%; Score 174; DB 5; Length 806;
83.7%; Pred. No. 8.8e-16;
live 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50176; ARM_REPEAT; 7.
SEQUENCE 806 AA; 90462 MW; 689E5E982CD5051A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 GNQESKLIILSSGGPAELVRIMRSYTYEKLLYTTCRVLKVLSV 408
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama T.;
"Identification of a Hydra homologue of the beta-
catenin/plashoglobin/armadillo gene family.";
Gene 172.155-159(1996).
EMBL; U36781; AAC47137.1; -.
HSSP; Q02248; 2BCT.
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Pfam; PF00514; Armadillo_seg; 10.
SMART; SM00185; ARM; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.78
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel.
C54D1.6 PROTEIN.
C54D1.6 OR BAR-1.
Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                   BETA-CATENIN.
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       DDT REP DE REP D
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Gaps
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NCBI_TaxID=6239;
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37.0%; Score 78.5; DB 5; Length 678;
Best Local Similarity 45.0%; Pred. No. 0.019;
Matches 18; Conservative 10; Mismatches 11; Indels
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Tue Jul 30 08:15:47 2002

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7;
                                                                             Length 364;
                                                                                     Indels
                                                                            Query Match

27.1%; Score 57.5; DB 17;
Best Local Similarity 39.5%; Pred. No. 8.2;
Matches 15; Conservative 7; Mismatches 9;
                                                                                                 1 GNQESKLIILASG-----GPQALVNIMRTYTYEKLL 31
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Search completed: July 29, 2002, 16:12:06 Job time: 476 sec

OM protein - protein search, using sw model Run on:

July 29, 2002, 16:07:54; Search time 158.47 Seconds (without alignments) 28.737 Million cell updates/sec

US-09-641-104A-9

Perfect score:

1 CSSNKPAIVEAGGMQALGLH.....TDPSQRLVQNCLWTLRNLSD 41 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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16: /SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
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18: /SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
19: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:*
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22: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:* A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Human beta-catenin	Human beta-catenin	Human beta catenin	Human beta-catenin	Novel human secret	Human beta-catenin	Mouse beta-catenin	Novel human secret	Cellular Receptor	Drosophila melanog	Drosophila melanog
	ID		AAY33220	AAY33235	AAB07290	AAY70740	AAU28118	AAE06038	AAE06039	AAU28306	AAR11354		
	DB	1 1 1	20	20	21	21	22	22	22	22	12	22	22
	Query Match Length DB]		41	41	781	781	781	781	781	800	700	840	840
oР	Query	111111	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	85.3	82.5	82.5
	Score		217	217	217	217	217	217	217	217	185	179	179
	Result No.	1	1	7	Э	4	S	9	7	8	6	10	11

ALIGNMENTS

AAY33220 RESULT

Ą. AAY33220 standard; peptide; 41

AAY33220;

(first entry) 18-NOV-1999 Human; beta-catenin protein armadillo repeat arm6 fragment.

modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; B-cadherin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ:regeneration; tissue regeneration; hair growth. Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1;

Homo sapiens.

DE19909251-A1.

26-AUG-1999.

.99DE-1009251. 22-FEB-1999; 98DE-1007390 21-FEB-1998; (DELB-) DELBRUECK CENT.MOLEKULARE MEDIZIN MAX.

Birchmeier W, Von Kries J;

NPI; 1999-470389/40.

Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor

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Example 4; Figus; 16pp; German.

suppressor gene products

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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-L/TCF+4 transcription factors, or their comprising part of the LEF-L/TCF+4 transcription factors, or their carmaillo domain (arm units 3-8) of beta-catenin, and mutants of the complete beta-catenin molecule, that include at least one of the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or specific interaction domains for LEF-1, TCF-4, APC, conductin or screening substance libraries for compounds that modulate interaction of screening substance libraries for compounds that modulate interaction of sea key compound in the Wnt signalling pathway and is involved in beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin is oncogenic but interaction with APC, conductin or E-cadherin is oncogenic (A) which inhibit interaction are particularly used to transcribe themselved to the colon and melanoma, but also, treat tumors, especifically carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and the catenin armadillo repeat fragments described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-catenin; human; armadillo repeat; treatment; human disease; LBF-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 217; DB 20; 100.0%; Pred. No. 9.3e-25;
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                                    Disclosure; Page 7; 16pp; German.
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Matches 41; Conservative
suppressor gene products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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This, invention, describes a novel agent (A) for treating human disease this, invention describes a novel agent (A) for treating human disease which; is based, on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of comprising part of the LEF-1/TCE-4 transcription factors, or their comprising part of the LEF-1/TCE-4 transcription factors, or their comprising part of the LEF-1/TCE-4 transcription factors, or their complete beta-catenin molecule, that include at least one of the complete beta-catenin molecule, that include at least one of the complete beta-catenin solered; the left of normal of left of the colon and melanoma, but also, there they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth, AAY3230-Y33241 represent mutant the left of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta catenin; cadherin; metastasis; cadherin-associated protein; human; colorectal cancer; melanoma; antisense oligonucleotide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB07290 standard; Protein; 781 AA
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Matches 141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human beta catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 41 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB07290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         κí.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a method of female primate contraception comprising administering an antagonist of a Wnt polypeptide, inhibiting occyte development. Wnt polypeptides are useful for promotive maturation of an immature occyte. Wnt polypeptides are also useful for increasing the number of mature occytes and to enhance occyte viability. Soluble fragments of Wnt polypeptides have the ability to inhibit Wnt signalling, e.g., by blocking binding of a naturally-occurring Wnt protein to its receptor. They may be used to generate monoclonal antibodies which can inhibit occyte development. The present sequence is the human beta-catenin protein. Dominant negative mutants of beta-catenin lack one
                                                 Beta catenin is a member of the catenin family of cytosolic proteins and a key member of the Wnt signalling pathway. Catenins interact with the cytoplasmic domains of cadherin glycoproteins, and are important in maintaining cell adhesiveness; The loss of cell adhesiveness is implicated in metastasis. Beta catenin is also known as cadherin-associated protein and is implicated in colorectal cancer and melanoma. The present sequence is the human beta catenin protein. The coding sequence of this protein was used in the present invention to design antisense oligonucleotides (AAA5827-AS8366). The oligonucleotides are capable of hybridising to human beta catenin, in order to inhibit expression of human beta catenin. The oligonucleotides may be used in gene therapy for colorectal cancer or melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contraceptive composition for inhibiting oocyte development in a female
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 217; DB 21; Length 781; 100.0%; Pred. No. 3.6e-23; Ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           primate comprises a Wnt polypeptide antagonist
                 Example 13; Columns 45-52; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY70740 standard; protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 26; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcmahon AP, Parr BA, Vaino S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US23640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0104355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-317845/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                         781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200021555-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY70740;
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY70740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel isolated human secreted polypeptides (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                        Gaps
or more armidillo-like repeats which participate in cadherin binding. Other mutants include those lacking amino acids 555-781 or 424-781,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ma Y, Zh.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted protein; arthritis; Crohn's disease; sepsis; shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel-polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders -
                                                                                                                                                        ö
                                                                                                                      Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu C, Wehrman T, nem. T, Thang J, Chen R, Xue AJ,
                                                                                                                                                        Indels
                                                                                                                                                                                                            350 cssnkpaiveaggmqalglhltdpsqrlvqnclwtlrnlsd 390
                                                                                                                    100.0%; Score 217; DB 21;
100.0%; Pred. No. 3.6e-23;
vative 0; Mismatches 0;
                                                                                                                                                                                 EL CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secretory protein, Seq ID No 287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID No 287; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                               AAU28118 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0574454.
2000US-0596193.
2000US-0616847.
2000US-0665363.
2000US-0693267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Asundi V,
Yang Y, Drmanac R<sup>5</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAR-2001; 2001WO-US04942
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                    41; Conservative
                                   or'1-422 of beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-589934/66.
                                                                                                                                    Best Local Similarity
Matches 41; Conserv
                                                                    781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200166689-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-2000;
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17:JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                 AAU28118;
                                                                     Sequence
                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                             RESULT
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Disclosure; Page 23-24; 33pp; English.

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the polypeptide as well as for studying modulators of the polypeptides.

(1) induces the proliferation of neural cells and regeneration of nerve

CC and brain tissue and is useful for the treatment of central and

peripheral nervous system diseases and neuropathies, such as Alzheimer's,

CC parkinson's disease, Huntington's disease, and amyotrophic lateral

CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

CC activity, regulation of haematopolesis and is useful for treating mayeloid

CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia

CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve

CI stague growth, and in tissue repair, healing of burns, incisions,

CL incers, for treating osteoporosis, osteoarthritis, bone degenerative

CL disorders or periodontal disease. Furthermore, (I) is also useful for

GL sorders, or periodontal disease. Furthermore, (I) is also useful for

CL disorders including severe combined immunodeficiency (SCID), bacterial or

CL disorders including severe combined immunodeficiency (SCID), bacterial or

CL disorders including severe combined immunodeficiency (SCID), bacterial or

CL disorders including severe combined immunodeficiency (SCID), bacterial or

CL disorders including severe combined immunodeficiency (SCID), bacterial or

CL disorders including severe combined immunodeficiency (SCID), bacterial or

CL disorders including severe combined immunodeficiency (SCID), bacterial or

CL disorders including severe combined immunodeficiency (SCID), acterial or

CL disorders including severe combined immunodeficiency (SCID), and and conditions, carbohydrate, vitamins, minerals, provides

CC reactions and conditions, carbohydrate, vitamins, minerals, provides

CC diservity and can act as an antigen in a vaccine composition to raise an

CC minume response. AAUSBOSD-AAUSBOSS represent novel human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of beta-catenin in the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient; signalling pathway; beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 217; DB 22; 100.0%; Pred. No. 3.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE06038 standard; Protein; 781 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human beta-catenin protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US01459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2000; 2000US-0176786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-465328/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nusse R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE06038
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The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell of mammalian concentration of beta-catenin in a progenitor or stem cell of which of which expanded sufficient for the progenitor or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells; aspanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or ineages. The expanded cell populations are also useful in transplantation to restore haematopoletic function to autologous or alignment of approach to the cellplants. The present sequence is human beta-catenin projetin. Beta-catenin is a pivoal player in the signalling pathway in this account of a several developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 217; DB 22;
100.0%; Pred. No. 3.6e-23;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 28-30; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STRD.) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE06039 standard; Protein; 781 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signalling pathway; beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reyart, Nusse R, Weissman IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse beta-catenin protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188-JAN-2000; 2000US-0176786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-465328/50.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       781 AA,
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                                                                                                                                                                                                                                                                                                                                        processes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Example 2; SEQ'ID No 663; 107pp; English.

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in an in vitro culture medium for a period sufficient for the progenitor or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoietic function to autologous or allogeneic recipients. The present sequence is mouse beta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway initiated by Wnt proteins, which are mediators of several developmental
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 781 AA;
                                                                                                                                                                                                                                                                                                                                                                     processes
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Gaps 0; 100.0%; Score 217; DB 22; Length 781; 100.0%; Pred. No. 3.6e-23; Indels 1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41 ; 0 Mismatches ö 41; Conservative Query Match Best Local Similarity Matches 41; Conserv ò g

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AAU28306 standard; Protein; 800 AA AAU28306

AAU28306;

18-DEC-2001 (first entry)

Novel human secretory protein, Seq ID No 663.

ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; fertility; analgesic; pain; antigen.

Homo sapiens.

WO200166689-A2.

13-SEP-2001

05-MAR-2001; 2001WO-US04942.

2000US-0574454. 2000US-0596193. 2000US-0519705 07-MAR-2000; 17-JUN-2000; 19-MAY-2000;

2000US-0616847. 2000US-0665363. 2000US-0693267 20-OCT-2000; 14-JUL-2000;

(HYSE-) HYSEQ INC.

ι F, Ma Y, Zhou P; Xue AJ, Wang J; В, Wehrman T, ng J, Chen C, Wehrma Zhang J, Asundi V, Xu Drmanac RT, WPI; 2001-589934/66. N-PSDB; AAS45206. Liu C, A Yang Y, Tang YT, Zhao QA,

Ren

"fragment most pref. included"

Binding-site Binding-site

/note= "fragment most pref. included"

Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -

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Inflammatory conditions such as arthritis, nephritis, cronn's olsease, cischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and candeling. (1); (11) and modulators of (11) are useful for creating transgenic animals useful for studying the in vivo activities of creating transgenic animals useful for studying the in vivo activities of creating transgenic animals useful for studying the in vivo activities of creating transgenic animals useful for studying modulators of the polypeptides. (1) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and coering the proliferation of neural cells and amyotrophic lateral extractions of slesase, Huntington's disease, and amyotrophic lateral coering sclerosis. In addition, (1) is involved in chemotactic or chemokinetic sclerosis. In addition, (1) is involved in chemotactic or chemokinetic cor lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of home, cartilage, tendon, ligament and/or nerve cellsorders, or periodontal disease. Furthermore, (1) is also useful for treating osteoporosis, osteoarthritis, bone degenerative disorders or periodontal disease. Furthermore, (1) is also useful for ceperfusion injury in various tissues, various immune deficiencies and clisques including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, creations and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorlythms or circadian cycles of rhythms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein
                             The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 217; DB 22; 100.0%; Pred. No. 3.7e-23;
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385..400
"note= "fragment pref. inlcuded"
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/note= "fragment pref. included"
303.309
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Best Local Similarity 100.00
Best Local Similarity 100.00
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Binding-site
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention 1 useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA, sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL1675) and the encoded proteins The Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo int/pub/published_pct_sequences.
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                                                                                                                                  igolated nucleic acid detection reagent for detecting 1000 or more strom Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                 Disclosure; SEÓ ID NO 7380; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 840;
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Pred. No. 1.7e-17;
3; Mismatches 4;
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                   Myers EW;
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Adams M, Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.9%;
Matches, 34; Conservative
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11-JUL-2000; 2000US-0614150
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                                                    WEE: 2001-656860/75
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N-PSDB; ABL09922
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                                                                                                                                                                            genes from Drose
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA segment encoding CR-2 ligand and CR2 binding site - used to treat auto-immune disease, B-cell lymphoma and inhibit Epstein-Barr virus infection
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Pred. No. 1.7e-18;
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2000US-0614150.
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89US-0404679.
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See also AAQ11140-42.
                                                                                                                               90WO-US05027
                                                                                                                                                                                                                                                                  INST BIOLOGIC
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                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-101864/14.
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Best Local Similarity
Matches 36; Conserv
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11-JUL-2000;
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08-SEP-1989;
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                              WO9103251-A
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capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                              specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                    the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                Indels
                                                                                                                 The sequence data for this patent did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 24255
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                                                                                                                                                                                                                                               Pred. No. 1.7e-17
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11-JUL-2000; 2000US-0614150.
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                                                                                                (ABB57737-ABB72072).
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                                                                                                                                                                                                                                              Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                840 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB65821;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                           ABB65821
                                                                                                                                                                                                                                                                                                                                                                          RESULT
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840 AA

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenomatous polyposis coli (APC)-2, and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSSNKPAIVEAGG-----35
                                                                                                                                                                                                                                    Adenomatous polyposis coli 2; APC-2; tumor suppressor; Wnt pathway;
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                        Indels
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                                               0.091;
0.091;
82.5%; Score 179; DB 22, 82.9%; Pred. No. 1.7e-17, 1ve 3; Mismatches
                                                                                                                                                                                                                                                                                                                         /note= "encoded by stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72.5; DB Pred. No. 0.0914; Mismatches
                                                                                                                                                                                                                                                                                             Location/Qualifiers
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Es JH, Pelfer MA, Clevers JC;
                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human tumor suppressor gene, used in the diagnosis, prevention,
                                                                                                                                    AAY92061 standard; Protein; 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 4; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.48;
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-NL00595
                                                                                                                                                                                                                                                                                                                                                                                                                          98EP-0203237
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYUT-) RIJKSUNIV UTRECHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query, Match
Best Local Similarity 32.3
Matches: 21, Conservative
                        Conservative
                                                                                                                                                                                                             Human APC-2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-293152/25.
N-PSDB; AAA08835.
          Similarity
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Misc-difference
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                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000.
                                                                                                                                                                                      01-AUG-2000
                        34;
                                                                                                                                                                                                                                                  cytostatic.
                                                                                                                                                             AAY92061;
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Query Match
Best Local S
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                        Matches
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سمد در اینها

(first entry)

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Identifying a substance that inhibits the interaction between a viral protein and a host cell protein, useful for the discovery of new antiviral compounds -
                                                                identification; antiviral; viral protein; viral replication; NP;
                                                  reast, host cell protein SRP1 SEQ ID NO:5.
                                                                                                                                                                           (MOUN') MOUNT SINAI SCHOOL MEDICINE.
AAB70385 standard; Protein; 542 AA.
                                                                                                                                                                                                                                                           Example; Fig 3; 147pp; English.
                                                                            viral infection; nucleoprotein.
                                                                                                                                           11-AUG-2000; 2000WO-US22257.
                                                                                          Saccharomyces cerevisiae.
                                                                                                                                                                                                           WPI; 2001-168816/17.
                                                                                                             WO200111335-A2.
                                                                                                                                                          11-Aug-1999;
                                   02-MAX-2001
                                                                                                                            15-FEB-2001
                                                                                                                                                                                             O'Neill R,
                 AAB70385;
     Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a human unc-5H81 cDNA, useful in yeast two hybrid experiments for identifying unknown human cDNAs which encode proteins that interact with the human unc-5C protein -
                                                                                                                             Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm; protein-protein interaction; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2274;
                                                                                                                                                                                                                                                      Bogaert T, Verwaerde P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67.5; DB 22;
Pred. No. 1.8;
5; Mismatches 16;
                                                                                                               Mouse APC-2 protein sequence SEQ ID NO:65.
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 185-192; 246pp; English.
                                                                AAB50674 standard; Protein; 2274 AA
                                                                                                                                                                                                                                                       Jan Criekinge W, Roelens I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.1%;
29.2%;
                                                                                                                                                                                                         02-JUN-2000; 2000WO-EP05108.
                                                                                                                                                                                                                       99GB-0012755
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.1
Best Local Similarity 29.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                        WPI; 2001-016508/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2274 AA;
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                                                                                                                                                                        WO200073328-A2.
                        716 lwnls 720
       36 LRNLS 40
                                                                                                                                                                                                                       01-JUN-1999;
                                                                                                 19-MAR-2001
                                                                                                                                                                                        07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                 AAB50674;
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Palese PM;

Harty R,

99US-0148263

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The present invention describes a method (M1) for identifying a substance that inhibits the interaction of a viral protein (VP) with a substance that inhibits the interaction of a viral protein (VP) with a host cell protein (HP). The method comprises: (a) contacting HP with VP in the presence of a test substance; and (b) detecting complex formation, where the ability of the test substance to inhibit HP/VP interaction is indicated by a decrease in complex formation. The antitizinal compounds in the interaction between a host protein (NSI-BP or NBI-1) and a viral protein (NSI) are useful for treating or inhibiting viral compounds include peptides and antibodies. In particular Antiviral compounds include peptides and antibodies. In particular compositions comprising a polypeptide containing an amino acid sequence corresponding to the NP-NLS domain of the influenza virus NP protein, which inhibits the specific interaction of the NPI-1 protein with the influenza viral infection in humans. The present sequence represents influenza viral infection in humans. The present sequence represents
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10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337'vinagvlpalrillsspkenikkeacwtisnit 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 IVEAGGMOALGLHLTDPSORLVQNCLWTLRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.1%; Score 61; D 30.3%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the present invention.
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 AA;
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Search completed: July 29, 2002, 16:07:55 Job time: 645 sec

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Indels

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1 CSSNKPAIVEAGG----

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RESULT 15 AAB70385

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, A Sequence 7, A Sequence 5, A Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16,
Sequence 16,
Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                     1 CSSNKPAIVEAGGMQALGLH......TDPSQRLVQNCLWTLRNLSD
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                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-628-145-7
US-08-179-738-5
US-08-179-738-5
US-08-628-145-10
US-08-179-738-2
US-08-179-738-2
US-08-179-738-3
US-08-179-738-3
US-08-179-738-3
US-08-628-145-2
US-09-510-654-4
US-09-510-654-4
US-09-510-654-4
US-09-510-654-4
US-08-933-227-4
US-08-933-227-4
US-08-289-548A-7
US-08-28-548-7
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-452-655B-2
US-08-452-655B-7
US-08-370-235A-2
US-08-450-582-2
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9-548A-2
                                                                                                                                                                       231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                   US-09-641-104A-9
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Score Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                          Scoring table:
                                      OM protein
                                                                                                                        Sequence:
                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                        Database
                                                           Run on:
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Gaps

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DB 1; Length 542; 13; Indels

Score 61; DB 1 Pred. No. 0.45; 10; Mismatches

28.1%; Sco. 30.3%; Prective 10;

Query Match Best Local Similarity Matches 10; Conserva

Conservative

LENGTH: 542 amino acids TYPE: amino acid

LENGTH:

STRANDEDNESS: single

unknown

; MOLECULE TYPE: protein US-08-246-583-3

8 IVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLS 40

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Sequence 3, Application US/08246583

Sequence 3, Application US/08246583

Patent NO. 5750394

GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: O'Neill, Robert
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION OF HOST CELL PROTEINS
TITLE OF INVENTION: AND VIRAL PROTEINS REQUIRED FOR VIRAL REPLICATION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
CITY: NEW YORK
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COUNTRY: U.S.A.

2 IP: 10036-2711
COMPUTER READBLE PORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/246,583
FILING DATE: 20-MAY 1994
CLASSIFICATION: 514
ATONREY/AGENT INPORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGERENCE/POCKET UNMBER: 30,742
TELECHONE: (212) 790-9900
                      US-08-821-355A-7
US-09-003-687A-7
US-09-103-687A-7
US-08-918-605-7
US-08-913-814-48
US-09-613-920-4
US-08-916-352-2
US-08-802-208-4
US-08-804-227C-14
US-08-804-198-2
US-08-804-198-2
US-09-565-910-3
US-09-565-910-3
                                                                                                                                                                                                                                                                                                                                                                                                US-08-246-361A-20
US-08-463-772-20
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                  RESULT 4
UG-08-179-738-5
Sequence 5, Application US/08179738
Fatent No. 5578462
GENERAL INFORMATION:
APPLICANT: Seizinger, Bernd R.
APPLICANT: Blanchl, Albert B.
TITLE OF INVENTION: No. 557846221 NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
STREET: 635 Bryant. Street
CITY: Palo Alto
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE-FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59.5; DB 2;
Pred. No. 0.83;
4; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 GMOALGLHLTDPSORLVONCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                          TELEFAX: (415) 327-328

TELEFAX: (415) 327-3231

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ. ID NO. 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUCREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/179,738
FILENG DATE: 10-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT'.INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Robins, Roberta L
REGISTRATION: NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid:
TOPOLOGY: linear'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
U.S.A :;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: murine US-08-628-145-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                  APPLICANT: Sciliger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Kley, Nikolai A.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5578462el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER, READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PPP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 10-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Seizinger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5872214el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
       337 VINAGVLPALRLLLSSPKENIKKEACWTISNIT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5998-0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: RObins, Roberta L.
REGISTRATION UNDRER: 33,208
REFERENCE/DOCKET UNDRER: 5998-
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 417-8999
TELEFAX: (415) 327-321
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-08-628-145-7
Sequence 7, Application US/08628145
Patent No. 5872214
GENERAL INFORMATION:
                                                                                                               Sequence 7, Application US/08179738
Patent No. 5578462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Reed & Robins
635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.2
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: murine US-08-179-738-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
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                                                                                                  US-08-179-738-7
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Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Seizinger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Blanchi, Albert B.
TITLE: GE INVENTION: No. 5872214el NF2 Isoforms
NUMBER OF SEQUENCES: 26
                                                                                                                                                       APPLICANT: Seizinger, Bernd R.
APPLICANT: Riey, Mikolai A.
APPLICANT: Bianchi, Albert B.
TITLE: OF INVENTION: No. 5872214el NF2 Isoforms
NUMBER OF SEQUENCES: 26
FILING DATE: 04 APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,738
FILING DATE: 10-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: RObins, ROberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GMOALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-628:145-5; Sequence: Sequence: S, Application US/08628145; Patent'No. 587214; GENERAL'INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .... 5
.....rutH: 591 amino acids
TYPE: amino acids
TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  Reed'& Robins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE: OF INVENTION: NO NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               ADDRESSEE: Reed'& R
STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-628-145-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                             Score 59.5; DB 1; Length 591; Pred. No. 0.85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,738
FILING DATE: 10-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.5; DB 1;
Pred. No. 0.85;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Seizinger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5578462el NF2 Isoforms
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                      |: ||||||: || || || || 235 GVDALGLHIXDPENRLTPKISFPWNEIRNIS 265
                                                                                                                                                                                                                                                                                                                                13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08179738 Patent No. 5578462 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: RODINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SED NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                              27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.48;
            TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                 LENGTH: 591 amino acids
TYPE: amino acid
                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 591 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.23
Matches 14; Conservative
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                        linear
                                                                                                                                                                                         murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94301
                                                                                                                                                                                       ; ORGANISM:
US-08-179-738-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM:
US-08-179-738-10
                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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ADDRESSEE:

13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40

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us-09-641-104a-9.rai

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Gaps
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0.85;
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Sequence 16, Application US/08478087
Setent No. 6077685
GENERAL'INFORMATION:
APPLICANT: AT TOTALLELY, James A.
APPLICANT: MACCOLLIN, M1a M.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Ressler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 59.5; DE
; Pred. No. 0.85;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brown, Anne
REGISTRATION, NUMBER: 36,463
REPERENCE/DOCKET, NUMBER: 0609,3850003
TELECOMMUNICATION: NPFORMATION:
TELEFONMUNICATION: 10203 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ. ID. NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING STSTEM: TO TOOL WESTERN TOOL WATER TIME APPLICATION DATE: 07 -070N-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATE: US 08/171,718
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB-1993
PRIOR APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MR-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MR-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: BOOWN, ANDE
                FILING DATE: 19.ANG-1993
PRIORIAPPLICATION DATA:
"APPLICATION NUMBER: US 08/022,034
"FILING DATE: 25 FEB-1993
PRIOR'APPLICATION DATA:
"APPLICATION NUMBER: US 08/026,063
FILING DATE: 04 MAR-1993
ATTORNEY/AGENT'INFORMATION:
APPLICATION NUMBER: US 08/108,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.4%; 45.2%;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.4'
Best Local Similarity 45.2'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-171-718-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        inear
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ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-08-478-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59.5; DB 2; Length 591; Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08171718
Patent No. 5707863
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Trofatter, James A.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                             CALIF: 94301

CALIF: 94301

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,145
FILING DATE: 04-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/179,738
FILING DATE: 10-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERE: 5998-0017
TELEPHONE: (415) 517-8999
TELEPHONE: (415) 517-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ALIDRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,718
FILING DATE: 22-DEC-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.48;
           635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.28
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA
         STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                                                                              U.S.A
                                                                                              94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-171-718-16
                                                                              COUNTRY:
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Score 59.5; DB 1; Length 596;
Pred. No. 0.86;
4; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL, INFORMATION:
APPLICANT: Seizinger; Bernd R.
APPLICANT: Kley, Nikolai A.
ARPLICANT: Blanchi, Albert B.
TITLE OF INVENTION: No. 5872214el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robins
STREET: 635 Bryant Street
                                                                                                                                                                                                     APPLICANT: Seizinger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Blanchi, Albert B.
TIŢLE OF INVENTION: No. 5578462el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                235 GVDALGLHIYDPENRLTPKISFPWNEIRNIS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 GVDALGLHIYDPENRLTPRISFPWNEIRNIS 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/179,738 FILING DATE: 10-JAN-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Robins, Roberta L.
REGISTRATION UNDRER: 33,208
REPERENCE/DOCKET UNDRER: 5998
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08628145
Patent No. 5872214
                                                                                                                                        Sequence, 3, Application US/08179738
Patent No. 5578462
                                                                                                                                                                                                                                                                                                                                     E: Reed & Robins
635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 27.4%;
Best Local Similarity 45.2%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT . INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 596 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Reed & F
STREET: 635 Bryant
CITY: Palo Alto
STATE: California
                                                                                                                                                                                    GENERAL, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT > 12
US-08-628-145-2
                                                                                                  RESULT . 11,
US-08-179-738-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-179-738-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 596;
                                                                                                                                                                                                                                                                                                               27.4%; Score 59.5; DB 3; Length 595; 45.2%; Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,738
FILING DATE: 10-JAN-1994
CLASSICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.5; DB 1;
Pred. No. 0.86;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Seizhinger, Bernd R.
APPLICANT: Kley, Nikolai A.
APPLICANT: Blanchi, Albert B.
TITLE OF INVENTION: No. 557846221 NF2 ISOforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
REGISTRATION NUMBER: 36,463
                                                                                                                                                                                                                                                                                                                                                                                                                           235 GVDALGLHIYDPENRLTPKISFPWNEIRNIS 265
                                                                                                                                                                                                                                                                                                                                                                                                13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08179738 Patent No. 5578462
                                REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Reed & Robins STREET: 615 Bryant Street CITY: Palo Alto STATE: California COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-331
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 27.4%;
Best Local Similarity 45.2%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 596 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.23
Matches 14; Conservative
                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-478-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-179-738-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-179-738-2
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13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40

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Gaps
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Patent No. 6027901
GENERAL INFORMATION:
APPLICANT: Shan, Bei
APPLICANT: Nitta, Masahiro
TITLE OF INVENTION: CYP7 Promoter-Binding Factors
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Shan, Bell
APPLICANT: Shan, Bell
TITLE, OF INVENTION: CYP7 Promoter-Binding Factors;
TITLE, OF INVENTION: CYP7 Promoter-Binding Factors;
FILE REFERENCE: T97-013
CURRENT APPLICATION NUMBER: US/09/132,619B
CURRENT FILING DATE: 1998-08-11
FEALIER'APPLICATION NUMBER: 60/067,708
FEALIER'APPLICATION NUMBER: 1997-12-08
NUMBER OF SEC ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                          27.4%; Score 59.5; DB 2;
45.2%; Pred. No. 0.86;
tive 4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5; DB; Pred. No. 2.3; 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136. KRALIRANGLKLEAMSQVDDQMKLLQNC-WS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 GVDALGLHIYDPENRLTPKISFPWNEIRNIS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' KPAIVEAGGMQALGLHLTDPSQRLVQNCLWT 35
                                                                                                                                                                                                                                                                                                                                                                                                                           13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/09132619B; Patent No. 5958697
              REFERENCE/DOCKET NUMBER: 5998
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415), 617-8999
TELEFAX: (415), 327-3231
INPORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENERA: 596 amino acids
TYPE: amino acid
REGISTRATION NUMBER: 33,208
                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                      Query Match 2/.4:
Best Local Similarity 45.29
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                     CRCANISM: Homo sapten US-08-628-145-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: human
US-09-132-519-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15.
US-09-282:803B-4
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US-09-132-519-4
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Pred. No. 0.86;
4; Mismatches 10; Indels
                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: 04-APR-1996
CLASSIFICATION NUMBER: 05/08/628,145
FILING DATE: 04-APR-1996
PRIOR APPLICATION NUMBER: 08/08/19,738
FILING DATE: 10-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5999-0017
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELEFRAME (415) 617-8999
TELEFRAME (415) 617-8999
TELEFRAME (415) 617-8399
TELEFRAME (415) 617-3231
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Selzinger, Bernd R.
APPLICANT: Bianchi, Albert B.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5872214el NF2 Isoforms
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GMQALGLHLTDPSQRLVQNCL--WT-LRNLS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,738
FILING DATE: 10-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAMM: RObins, Roberta L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08628145
Patent No. 5872214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.4%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 596 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.28
Matches 14; Conservative
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 635 Bryant
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04 CLASSIFICATION:
      U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-628-145-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-628-145-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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us-09-641-104a-9.raj
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datamil Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,803B
FILING DATE:
CLASSIPICATION NUMBER: 36,627
NAME: OSMAN RICHARD A
REGISTRATION NUMBER: 797-013
FELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARCTRISTICS:
LENGTH: 323 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-282-803B-4

QUETY MATCh

RESPONDED TO CONSERVATIVE B; MISMATCHES 1; Indels 1; Gaps 1;
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5 KPAIVEAGGMQALGLHLTDPSQRLVQNCLWT 35 | 1:: | :| :| |:: | :| |:: | 136 KKALIRANGLKLEAMSQVDDQMKLLQNC-WS 165

δ Q Search completed: July 29, 2002, 16:05:10 Job time: 480 sec

> 4. January

.

4.5 Compugen Ltd. GenCore version Copyright (c) 1993 - 2000

- protein search, using sw model OM protein

July 29, 2002, 16:09:13 ; Search time 70.63 Seconds Run on:

(without alignments) 55.779 Million cell updates/sec

US-09-641-104A-9 217 1 CSSNKPAIVEAGGMQALGLH.....TDPSQRLVQNCLWTLRNLSD Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	beta-catenin - hum	beta-catenin - mou	beta-catenin - Afr	plakoglobin - mous	plakoglobin - Afri	plakoglobín, desmo	armadillo segment	hypothetical prote		hypothetical prote	0	beta-catenin - Cae	Õ	SRP1 protein - yea	overgrown hematopo	merlin protein - m	neurofibromin 2 -	merlin - mouse	icl containing pro		arm repeat contain	ferrichrome-bindin	nuclear localizati	pendulin - mouse	m-importin (nuclea	conserved hypothet	adenomatous polypo	adenomatous polypo	hypothetical prote
SUMMARIES	ΩI	A38973	S35091	835099	S35092	S35093	A32905	T12689	S33794	JC4835	S33793	T43175	T23341	T30258	S30884	A57319	I54368	833809	168664	A97433	AB2651	T45588	AB0527	A56516	S57873	S57345	C69052	RBHUAP	I49505	AI2246
	DB	7	7	7	7	~	~	7	~	7	7	7	7	7	7	7	7	7	7	~	~	7	7	7	~	~	~	-	7	7
	Match Length	781	781	781	621	738	744	843	820	806	817	811	678	2274	542	522	591	595	296	434	434	099	296	529	529	529	564	2843	2845	242
, , ,	Match	100.0	100.0	96.3	85.3	85.3	85.3	82.5	81.1	79.7	67.1	35.5	32.5	31.1	28.1	27.6	27.4	27.4	27.4	26.3	26.3	25.8	25.3	24.9			24.9	24.7	24.7	24.4
	Score	217	217	209	185	185	185	179	176	173	145.5	77	70.5	67.5	61		σ	59.5	6	57	57	26	22	54	54	24	54	53.5	53.5	23
+[::00	NO.	1	7	m	4	5	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

	env polyprotein pr	conserved hypothet	protein-glutamine	gene p120 protein	hypothetical prote	RAE-28 - mouse	gene C10 protein -	dynamin-like prote	hypothetical prote	transcription fact	probable protein p	paired box transcr	abrin-b precursor	abrin-d precursor	abrin-c precursor	hypothetical prote	
	B31479	E69532	2 A45321	S28498	: T00518	153172	149555	: T47968	: AI2516	S07896	: T00750	3 A60086	S32430	S32431	s S16022	G90570	
	24.4 . 273 2	24:4 298		24.4 911	24.2 924 2	24.2 1012 2		24.0 . 627 2	24.0 688 2	24.0 760 1	23.7 4.404 2	23.7 415 2	23.7 527 2	23.7 · 528 2	23.7 562 2	23.5 625 2	
er de	30 1 23	31 2 1 53	32 44 53	33. 5 53	34,17,52.5	35 . 52.5	36 52	37 35 36 52	38 1 52	39 🦸 52	40 - 51.5	41 : 51.5	42, 51.5	43 51.5	44., 51.5	45 51	

ALIGNMENTS

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A Status: preliminary
A Status: preliminary
A Status: preliminary
A Molecule type: mRNA
A Cross_references: EMBL:X87838; NID:91154853; PIDN:CAA61107.1; PID:9860988
C;Comment: The cytoplasmic protein beta-catenin normally binds to a region in the cyt
microfilament network.
C;Comment: Cellular levels of beta-catenin are regulated in part by the adenomatous p
C;Genetics:
                                                                              C;Species: Homo sapiens (man)
C;Date: 26;Jan-1996 #sequence_revision 08-Feb-1996 #text_change 08-Oct-1999
C;Accession: A38973; S55356; S31988
R;Huelsken, J.; Birchmeier, W.; Behrens, J.
O Cell Biol. 127, 20671-2069, 1994
A;Title: E-cadherin and APC compete for the interaction with beta-catenin and the cyt
A;Reference number: A38973; MUID:95105247
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A38973.
A; Accession: A38973.
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA.
A; Residues: 1-781 < HUE>
A; Cross-references: GB:Z19054; NID:g38519; PIDN:CAA79497.1; PID:g38520
A; Cross-references: GB:Z190664; NID:g38519; PIDN:CAA79497.1; PID:g38520
A; Experimental source: placenta
B; Nollet; F.; Berx, G.; Molemans, F.; van Roy, F.
B; Nollet; F.; Berx, G.; Molemans, F.; van Roy, F.
A; Nollet; B.; Sapiens beta-catenin mRNA.
A; Reference number: S55356
A38973 .
beta-catenin
```

ö C;Species: Mus musculus (house mouse) C;Date:∵06.Jan-1995 #sequence_revision 06.Jan-1995 #text_change 05-Nov-1999 C;Accession: S35091 Gaps ö 100.0%; Score 217; DB 2; Length 781; 100.0%; Pred. No. 2.6e-21; tive 0; Mismatches 0; Indels A; Gene: CDB:CTNNB1; CTNNB...
A; Cross-references: GDB:141922; OMIM:116806
A; Map position: 3p22-3p21:3
A; Map position: 3p22-3p21:3
C; Keywords: apoptosis: carcinogenesis; cell adhesion; cytosol F; 151-676/Region: 40-residue repeats 350 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 390 · · 1 · CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41 Best Local Similarity 100.0 Matches 41; Conservative beta-catenin - mouse Query; Match RESULT 1. 2 \$35091 δ Dp

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west.

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Discoglobin, desmosomal - human C;Species: Homo saplens (man) C;Species: Homo saplens (man) C;Species: Homo saplens (man) C;Species: Homo saplens (man) C;Species: Anov-1989 #sequence_revision 22-Nov-1989 #text_change 29-Aug-1997 C;Accession: A32905.
R;Franke, W.W.; Goldschmidt, M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cow Proc. Natl. Acad. Sci. U.S.A. 86, 4027-4031, 1989 A;Title: Molecular cloning and amino acid sequence of human plakoglobin, the common fareference number: A32905; MUID:89264555
                                                                                  placed by African clawed frog control of the contro
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N;Alterrate names: protein 86E4.6
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13. Aug-1999 #sequence_revision 13. Aug-1999 #text_change 21-Jul-2000
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Pred. No. 5.5e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted to the EMBL Data Library, June 1992
A, Reference number: S24636
A; Accession: S24636
A; Accession: S24636
A; Molecule: preliminary
A; Molecule: 133-184, V/,186-225, T/,227-292 < DEM>A; Cross-references: EMBL:X67078; NID:965253; PID:965253
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Best Local Similarity 87.8%;
Matches ; 36; Conservative
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A;Cross_references: GDB:126565;
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Best Local Similarity 87.0%
Local Similarity 87.0%
Local 36; Conservative
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A; Residues: 1.744 <FRA>
A; Cross-references: GB:M23410
C; Genetics:
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C; Keywords: cytoskeleton:
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A;Title: A homolog of the armadillo protein in Drosophila (plakoglobin) associated with A;Reference number: $35099; MUID:92073903
A;Accession: $35099
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995_#text_change 17-Mar-1999
C;Accession: S35092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Xenopus laevis (Africañ clawed frog)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
R;Butz, S.; Stappert, J.; Weissig, H.; Kemler, R. Science 257, 1142-1144, 1992
A;Title: Plakkoglobin and beta-catenin: distinct but closely related.
A;Reference number: S35091; MUID:92376536
A;Recession: S35091
A;Status: preliminary
A;Molecule type: MRNA
A;Residues: 1-781 < BMIS.
A;Residues: 1-781 < BMIS.
C;Keywords: cytoskeleton
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A;Residues: 1.781 CMC>
A;Cross-references: 68.M77013; NID:g214020; PIDN:AAA49670.1; PID:g214021
C;Keywords: cytoskeleton
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A;Title: Plakoglobin and beta-catenin: distinct but closely related. A;Reference number: 835091; MUID:92376536
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Pred. No. 4.6e-17;
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Pred. No. 2.6e-21;
0; Mismatches 0;
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Pred. No. 3.2e-20;
0; Mismatches 1.
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ilarity 100.0%;
Conservative 0
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87.8%;
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ilarity 97.6%;
Conservative
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C; Keywords: cytoskeleton
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Best Local Similarity
Matches 36; Conserv
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Best Local Similarity
Matches 40; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-621 < BUT>
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Best Local Similarity
Matches 41; Conserv
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armadillo protein homolog BAR-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-12000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43175; T28813
R;Eisenmann, D.M.; Maloof, J.N.; Simske, J.S.; Kenyon, C.; Kim, S.K.
Submitted to the EMBL Data Library, May 1998
A;Bescription: The beta-catenin homolog BAR-1 and LET-60 Ras coordinately regulate th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1173, 337-341, 1993
A;Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two in
A;Reference number: S33793; MUID:93305730
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A;Map-position: X
A;Introns:'23/2; 65/3; 97/3; 132/3; 181/3; 223/2; 261/3; 332/3; 414/3; 452/3; 500/3;
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A;Experimental source: strain Bristol N2; clone C54D1
                                           A;Cross'references: GB:U36781; NID:g1407600; PIDN:AAC47137.1; PID:g1407601
C;Comment: This protein plays roles in cadherin-mediated cell adhesion and
C;Genetics:
A;Gene: betaCtn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Urechis caupo
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
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A;Description: The sequence of C. elegans cosmid C54D1.
A;Reference number: 220527
A;Accession: T28813
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                                                                                                                                                                                                            Score 173; DB 2; I
Pred. No. 2.6e-15;
2; Mismatches 5;
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A;Molecule type: mRNA
A;Residues: 1-811 <EIS>
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R;Minx, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - spoonworm (Urechis caupo)
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                                                                                                                                                                                                               79.7%;
82.9%;
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73.28;
                                                                                                                                                                                                                                  Best Local Similarity 82.9
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 30; Conserv
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A: Residues: 1-811 <MIN>
                              1-806 <HOB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-817 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S33793
R; Rosenthal, E.
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession:
                              A; Residues:
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                                                                                                                                                                                                    A; Residues: 1-843 <FER>
A; Cross-references: EMBL:AL021106; NID:e1371406; PID:e1249776; PIDN:CAA15946.1
A; Cross-references: EMBL:AL021106; NID:e1371406; PID:e1249776; PIDN:CAA15946.1
B; Experimental source: clone cosmid 63B12
B; Riggleman, B:: Wieschaus, E:: Schedl, P.
Genes Dev. 3, 96-113, 1989
A; Title: Molecular analysis of the Armadillo locus: uniformly distributed transcripts an A; Reference number: A31861; MUID:89211895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1173, 337-341, 1993
Affilte: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver
A;Reference number: S33793; MUID:93305730
A;Accession: S33794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: JC4835
R; Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T.
R; Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T.
R; Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T.
A; Title: Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadillo
A; Reference number: JC4835; MUID: 96257271
A; Accession: JC4835
A; Status: nucleic acid sequence not shown
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                R.Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G. submitted to the EMBL Data Library, January 1998
A.Description: Sequencing the distal X chromosome of Drosophila melanogaster. A.Reference number: 217572
A.Recession: T12689
A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-catenin - Hydra magnipapillata
C;Species: Hydra magnipapillata
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ypothetical protein - sea urchin (Tripneustes gratilla)
.Species: Tripneustes gratilla
.bate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X54468; NID:g7610; PIDN:CAA38350.1; PID:g7611
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 CSSNKPAIVDAGGMOALAMHLGNMSPRLVONCLWTLRNLSD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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Pred. No. 4.2e-16;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSSNKPAIVEAGGMQALGLHLTDPSORLVONCLWTLRNLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 176; DB 2;
Pred. No. 1e-15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: FlyBase:FBgn0000117
A;Introns: 11/1; 557/3; 624/3; 715/3; 748/1
A;Note: 8684.6
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.1%;
82.9%;
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82.9%;
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Best Local Similarity 82.9
Matches 34; Conservative
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C; Accession: T12689; A31861
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A31861
A; Molecule type: DNA
A; Residues: 1-843 <RIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-820 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein
                                                                                                                                                                              Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S33794
R;Rosenthal, E.
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Asylata

Overgrown hematopoietic organs-31 tumor suppressor OHO31 - fruit fly (Drosophila mela

C; Species: Drosophila melanogaster

C; Date: OB-Dec-1995 #sequence_revision OB-Dec-1995 #text_change 17-Nov-2000

C; Accession: A57319; A57320; S57344

R; Toercek, I.; Strand, D:; Schmitt, R.; Tick, G.; Toercek, T.; Kiss, I.; Mechler, B.M.

J; Cell'Biol. 129, 1473-1489, 1995

A; Title: The overgrown hematopoietic organs-31 tumor suppressor gene of Drosophila en

A; Reference number: A57319; MUID:95310330

A; Status: preliminary

A; Molecule.type: DNA

A; Residues: 1-522 <TOE>

A; Cross-references: GB:X85752; NID:92511638; PIDN:CAA59753.1; PID:9755726

R; Kuessel, P; Frasch, M.

J; Cell'Biol. 129, 1491-1507, 1995

A; Title: Pendulin, a Drosophila protein with cell cycle-dependent nuclear localization

A; Reference number: A57320; MUID:95310331

A; Accession: A57320; MuID:95310331

A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:91302178; PIDN:CAA96083.1; PID:91302179; MIPS:YN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      temperature-sensitive
                                                                                                                                                                                                                                                                                RESULT [14]
S30884
SYND protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein N1606; protein YNL189w
C; Species: Saccharomyces cerevisiae
C; Dete: 28-May-1993 **sequence_revision 28-May-1993 *text_change 20-Jun-2000
C; Date: 38-May-1993 **sequence_revision 28-May-1993 *text_change 20-Jun-2000
C; Date: 38-May-1993 **sequence_revision 28-May-1993 *text_change 20-Jun-2000
C; Date: 38-May-1993 **sequence_revision 06 May-1993 *text_change 20-Jun-2000
C; Date: 38-May-1993 **sequence_revision 06 SRP1, a suppressor of temperature-sension of carracterization of SRP1, a suppressor of temperature-sension 30884
A; Reference number: 330884; MUID: 93070765
A; Residues: 1-542 cyan>
A; R
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                                                              582 COGNSLAVIESGGGILRNVSSLIATREDYRQVLRDHNCLQTLLQHLTSHSLTIVSNACGT 641
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-MOALGLHLTDPSQRLVQNCLWT 35
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A;Cross-references: SGD:SO005133; MIPS:YNL189w
A;Map position: 14L
C;Superfamily: pendulin
C;Keywords: nucleus; transmembrane protein
C;Steywords: nucleus; transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 VINAGVLPALRILLSSPKENIKKEACWTISNIT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 8 IVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLS 40
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A; Residues: 1-68, 'P', 70-522 <KUE>
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Best Local Similarity 30.39
Matches 10; Conservative
      1 CSSNKPAIVEAGG
                                                                                                                                                                                               642 LWNLS 646
                                                                                                               36 LRNLS 40
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N;Alternate names: APC2 protein
C;Species: Wus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T30258
R;van Es, J.H.; Kirkpatrick, C.; van de Wetering, M.; Molenaar, M.; Miles, A.; Kuipers, Curr. Biol. 9, 105-108, 1999
A;Title: Identification of APC2, a homoloque of the adenomatous polyposis coli tumour su A;Reference number: 220796; MUID:99147086
A;Accession: T30258
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-678 cMIL.)
A; Cross-references: EMBL:281564; PIDN:CAB04572.1; GSPDB:GN00019; CESP:K05C4.6
A; Experimental source: clone K05C4
B; Experimental source: clone K05C4
R; Costa, M.; Raich, W.; Agbunag, C.; Hardin, J.; Priess, J.R.
A; Costa, M.; Raich, W.; Agbunag, C.; Hardin, J.; Priess, J.R.
A; Description: A putative catenin-cadherin system mediates morphogenesis of the C. elegals A; Reference number: 222085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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A;Introns: 47/3; 78/1; 138/2; 174/3; 212/3; 238/3; 271/3; 396/1; 428/1; 474/3; 500/3;
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A;Molecule type: DNA
A;Residues: 1-2274 <VAN>
A;Cross-references: EMBL:AJ130783; NID:g4210431; PIDN:CAA10207.1; PID:g4210432
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C.Accession: T23341; T4221
R.Harris, B.
Submitted to the EMBL Data Library, November 1996
A.Reference number: 219729
A.R.Accession: T23341
A.Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                            Gaps
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          Length 811;
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                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 CPSNKPALISLGCLPALYVELCTAKDERSQTAILVAMRNLSD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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                                                                         13;
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Pred. No. 1.7;
5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.5; DB 2;
Pred. No. 0.19;
6; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSSNKPAIVEAGGMQALGLHL-TDPSQRLVQNCLWTLRNLSD
          DB 2;
0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ: Wolecule type: mRNA
Residues: 1-678 <COS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-creferences: EMBL:AF016853; PIDN:AAB94552.1
C;Genetics: A, Gene: hmp-2; CESP:K05C4.6
A, Map position: 1
A;Introns: 14/1; 235/1; 290/1; 620/3
                                                                                                                                                                              335 PNLVAFGGRQILANLLSHGSPRLVQSTLETLRNISD 370
   Score 77; DB 2, Pred. No. 0.03; 4; Mismatches
                                                                                                                                        6 PAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                                                                                                                                                                                                                                                          beta-catenin - Caenorhabditis elegans
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42.9%;
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29.28;
          35.5%;
52.8%;
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Matches 19; Conserv
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us-09-641-104a-9.rpr

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A:Cross-references: EMBL:U12269; NID:9555820; PIDN:AAA85260.1; PID:9555821
R:Kuessel, P.; Frasch, M.
Mol. Genet. 248, 331-363, 1995
A:Title: Yeast Srpl, a nuclear protein related to Drosophila and mouse pendulin, is requested number: S57866; MUID:96004702
A:Reference number: S57866
A:Reference number: S57866
A:Status: Preliminary; nucleic acid sequence not shown
A:Residues: 1-68, P',70-522 < KU2>
A:Ross-references: EMBL:U12269; NID:9555820; PIDN:AAA85260.1; PID:9555821
A:Cross-references: FlyBase:Pen
A:Cross-references: FlyBase:Fpn
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Q O Search completed: July 29, 2002, 16:09:14 Job time: 724 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 16:09:53 ; Search time 34.24 Seconds (without alignments) 46.364 Million cell updates/sec Run on:

US-09-641-104A-9 217 1 CSSNKPAIVEAGGMQALGLH.....TDPSQRLVQNCLWTLRNLSD 41 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES		
Result No.	Score	Query	Length	DB	QI	Description	
1	5 217	100.0		-	CTNB_HUMAN	P35222 homo sapien	ien
7	217	100.0		Н	CTNB_MOUSE	8 mus m	ılu
m	210	96.8		-	CTNB_RAT	Q9wu82 rattus norv	orv
4	209	96.3		П	CTNB_XENLA	xenobns	lae
S	. 191	88.0		-	ARM_MUSDO	_	nes
9	185	85.3		~~	PLAK_MOUSE	Q02257 mus musculu	ılu
7	185	85.3	738	-	PLAK_XENLA	P30998 xenopus lae	lae
æ	185	85.3		-	PLAK_HUMAN		ien
6	179	82.5		-	ARM_DROME		la
10	176	81.1		٦	CTNB_TRIGR	P35223 tripneustes	res
11	145.5	67.1		٦	CTNB_URECA		can
12	61	•	542	Н	IMA1_YEAST		nyc
13	9	27.6	522	П	IMA_DROME	P52295 drosophila	la_
14	59.5	27.4	595	П	MERL_HUMAN	P35240 homo sapien	ien
15			596	-	MERL_MOUSE	mus m	ılu
16	54		529	Н	IMA2_HUMAN	homc	ien
17	54	24.9	529	-	IMA2_MOUSE	mus m	n]n
18	54		764		TGLH_TACTR		ıs
19	S	24.9		-	PKP4_HUMAN		ien
20	e,	24.7		-	APC_RAT	ratto	orv
21	53.5	24.7		-	APC_HUMAN	P25054 homo sapien	ien
22	m.	24.7		-	APC_MOUSE	mus m	ılu
23	. 53	24.4		-	ENV_FLVC1	P21444 feline leuk	ank
24	23	24.4		-	CTD1_MOUSE	_	ոյո
25	53	24.4		-	CTD1_HUMAN	O60716 homo sapien	ien
26	52	24.0		-	SY06_MOUSE	4	ոլո
27	52	24.0		-	CGD1_CHICK	P55169 gallus gall	311
28	S	4		Н	OCT1_XENLA	3	lae
29	51.5	က	415	-		P32114 mus musculu	nlu
30	•	23.7	416	Н	- 1	Q02962 homo sapien	ien
31	51.5	23.7	527	Н		abrus	preca
32	51.5	23.7	562	-	ABRC_ABRPR	abrus p	preca
33	51	23.5	668	Н	ENV_FLVC6	3 feline	leuk

P14859 homo sapien	Q29076 sus scrofa	P11140 abrus preca	P08395 escherichia	Q14524 homo sapien	Q9z9p2 bacillus ha	P17065 saccharomyc	Oguq90 homo sapien	013864 schizosacch	P22339 mus musculu	P03392 feline sarc	feline			
OCT1_HUMAN	OCT1_PIG	ABRA_ABRPR	SPPA_ECOLI	CIN5_HUMAN	GRK_BACHD	SEC2_YEAST	PGN_HUMAN	IMB1_SCHPO	G45B_MOUSE	ENV_FSVST	ENV_FLVLB		ALIGNMENTS	
Н	Н	-	Н	П	Н	٦	-	Н	Н	-	Н			
23:5 ,743										22.6 534	22.6 662			
 340.8	35 51	36 5750.5	37:1 50.5	38,181 50	39: 49.5	40.49.5	41 1.4.49.5	42 . 49.5	43 49	44 49	45 4 49	5 A	 , T.	

ALIGNMENTS

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MEDLINE-20337986; 'PubMed-10882138;
                                   alpha catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTNB_RAT
Q9WU82;
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CTNB_RAT
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                              InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
BARRT; SM00185; ARM; 11.
PROSITE: PS50176; ARM; EPERAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
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X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 118-149 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-92376536; PubMed=1509266;
Butz S., Stappert J., Weissig H., Kemler R.;
"Plakoglobin and beta-catenin: distinct but closely related.";
Science 257:1142-1144(1992).
                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                     100.0%; Score 217; DB 1; Length 781; 100.0%; Pred. No. 1.9e-21; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Regulation of beta-catenin signaling in the Wnt pathway.";
Biochem. Biophys. Res. Commun. 268:243-248(2000).
                                                                                                                                 ARM 1.
ARM 2.
ARM 3.
ARM 4.
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ARM 9.
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ARM 10.
ARM 11.
ARM 11.
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                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      781 AA
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                                                                                                                                                                                                                                                                                                                                                                               002248;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                             85496 MW;
                           EMBL; X87838; CAA61107.1; -. EMBL; Z19054; CAA79497.1; -.
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Best Local Similarity 100.
Matches 41; Conservative
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389
441
484
530
571
666
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                                             PIR; S31988; S31988.
PDB; 1G3J; 17-JAN-01.
TRANSFAC; T02872; -.
MIM; 116806; -.
                                                                                                                              ructure
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                                                                                                                                                                                                                                                                                                                                                                                                                           CINNB1 OR CAINB.
                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-catenin.
                                                                                                                             Repeat; 3D-st
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                                                                                                                                                                                                                                                                                                                                                                        CTNB_MOUSE
                                                                                                                                                                                                                                             SEQUENCE
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CTNB_MOUSE
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11. MOIL CELLUIL...

MOIL CELL DISSISSA-543 (2000).

SIGNAL TRANSDUCTION THE REGULATION OF CELL ADHESION AND IN

SIGNAL TRANSDUCTION THROUGH THE WAT PATHWAY.

SIGNAL TRANSDUCTION THROUGH THE WAT PALLOWS THE STIMULATION

SIGNAL TRANSDUCTION THROUGH THE WAT PALLOWS THE STIMULATION

C. ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND

C. E-CADAPHERIN. THE NUCLEER FORM BINDS TCFLEF-1 AND MAY ALSO BIND

C. PONTINS AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND

C. PONTINS AND DUPLIN. CAN HETERODIMERIZE WITH ALCHA-CATENIN AND

C. STABLILLE CADHERIN COMPLEX TO THE CORTICAL ACTIN CATOSKELETON.

C. STABLILLED (LOW LEVEL. OF PHOSPHORYLATION).

C. PTM: PROBABLY PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS

STABLILLED (LOW LEVEL. OF PHOSPHORYLATION).

C. PTM: PROBABLY PHOSPHORYLATION).

C. PTM: PROBABLY PHOSPHORYLATION OF GSK-3B. PHOSPHORYLATION OF BETA-

C. PTM: RESULTING IN ITS ACCUMULATION IN CYTOPLASM.

RESULTING IN ITS ACCUMULATION IN CYTOPLASM.

C. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.

C. SIMILARITY: CONTAINS 12 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use. by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@lsb-sib.ch).
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PDB: 2BCT: 15-0CT-97.

PDB: 3BCT: 15-0CT-97.

PDB: 3BCT: 19-0V9-97.

PDB: 1DCW: 12-JUL-00.

TRANSFAC: T02984: -.

PDB: 1DCW: 12-JUL-00.

TRANSFAC: T02984: -.

PCB: 1PR000225: Armadillo.seg: 12.

SWART: SW00185: ARW: 11.

SWART: SW00185: ARW: 11.

SWART: SW00186: ARW: 11.
Pokutta S., Weis W.I.; "Structure of the dimerization and beta-catenin-binding region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Matches 41; Conservative
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350 CSSNKPAIVEAGGMQALGPHLTDPSQRLVQNCLWTLRNLSD 390 1) CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41

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                                                                                                                                                                                                                                                           J. Ceil. Physiol. 181:258-272(1999).

-!- FUNCTION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN SIGNAL TRANSDUCTION THROUGH THE WIT PATHWAX (BY SIMILARITY).

-!- SUBGINIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND B-CADHERIN. THE MUCLEAR FORM BINDS TCF/LEF-1 AND MAY ALSO BIND PONTINES AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND ALSO FORM A TRIMBRIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX TO THE CORTICAL ACTIN CYTOSKELETON (BY
                                                                                                                                                                              STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
MEDLINE=99428593; PubMed=10497305;
Chung S.S.W., Lee W.M., Cheng C.Y.;
"Study on the formation of specialized inter-Sertoli cell junctions in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: CYTOPLASMIC WHEN IT IS UNSTABILIZED (HIGH LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS TYBELLIZED (LOW LEVEL OF PHOSPHORYLATION) (BY SIMILARITY). TISSUE SPECIFICITY: EXPRESSED IN THE TESTIS.

DEVELOPMENTAL STAGE: HIGHLY EXPRESSED AT E30-60 DAY DPC IN THE TESTIS. REDUCED EXPRESSION AT E90 DAY DPC.
                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PROBABLY PHOSPHORYLATED BY GSK-3B. WNT-DEPENDENT ACTIVATION OF DVL ANTAGONIZES THE ACTION OF GSK-3B. PHOSPHORYLATION OF BETA-GATBUNI S REDUCED AND THE PROTEIN IS NO LONGER DEGRADED, RESULTING IN ITS ACCUMILATION IN CYTOPLASM (BY SIMILARITY) SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
SIMILARITY: CONTAINS 12 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
BARAT; SW00185; ARM; 11.
PROSITE; PS50176; ARM; 11.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9C29186B6DD54B87 CRC64;
                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0.00
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     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85454 MW;
 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
193
235
277
319
361
440
442
489
531
534
637
16-ocr-2001 (Rel.
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                  Beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                  ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
                                                                                                                                                                                                                                                                                                                                                                SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION PROPERTIES. ESSENTIAL COMPONENT OF THE VERTEBRATE WNT-SIGNALING PATHWAY AND IS REQUIRED FOR FORMATION OF THE EMBRYONIC AXIS. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                          MEDLINE-92073903; PubMed-1962194;
McGrea P.D., Turck C.W., Gumbiner B.M.;
"A homolog of the armadillo protein in Drosophila (plakoglobin)
associated with E-cadherin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3ECD27232239F799 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 209; DB 1;
Pred. No. 2.3e-20;
                                                        01-MAR-1992 (Rel. 22, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
               781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                       Xenopus laevis (African clawed frog)
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ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 9.
ARM 9.
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SMART; SM00185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, Q02248; 2BCT.
TRANSFAC; T03026; -.
InterPro; IPR000225; Armadillo.
                                            (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 96.3%;
Best Local Similarity 97.6%;
Matches 40; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M77013; AAA49670.1; -.
                                                                                                                                                                                                                                                                                         Science 254:1359-1361(1991).
              :STANDARD;
                                                                                                                                                     Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S35099; S35099.
HSSP; Q02248; ZBCT.
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                                                                                                                                                                 NCBI_TaxID=8355
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351
391
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REPEAT 14
                                                                                           Beta-catenin.
                                                                                                                                                     Xenopodinae;
                                                                                                                                                                                                                 TISSUE-Brain
                                             01 - MAY - 1992
                 CTNB_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE
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CTNB_XENLA
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Gaps

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ch 96.8%; Score 210; DB 1; Length 781; 1 Similarity 97.6%; Pred. No. 1.7e-20; 40; Conservative 0; Mismatches 1; Indels

Best Local Similarity Matches 40; Conserv

Query Match

0; Mismatches

Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

621 AA.

STANDARD;

g

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MEDLINE-92376536; PubMed-1509266;
Butz S., Stappert J., Weissig H., Kemler R.;
"Plakoglobin and beta-catenin: distinct but closely related.";
Science 257:1142-1144(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSOCIATED FORM.
-!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-!- SIMILARITY: CONTAINS AT LEAST 9 ARM REPEATS.
                                                 01-00r-1993 (Rel. 26, Created)
01-00r-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Jünction plakoglobin (Desmoplakin III) (Fragment)
                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                REVISIONS TO 294 AND 296.
                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=10090;
                      PLAK_MOUSE
Q02257;
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REPEAT
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           PLAK_MOUSE
                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web yn ono-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Musca.
                                                                                                                                                                                                                                                                                                                                               housefly Musca domestica.";
J. Mol. Evol. 36:224-233(1993).
-!- FUNCTION: SEGMENT POLARITY PROTEIN. MUTATION IN ARM PRIMARLLY
AFFECT THE POSTERIOR PART OF THE SEGMENT AND LEAD TO THE
PRODUCTION OF ANTERIOR STRUCTURES WITHIN THIS REGION. MAY BIND
A CADHERIN AND PARTICIPATE IN THE TRANSMISSION OF DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                    Peifer M.A., Wieschaus E.; The product of the Drosophila melanogaster segment polarity gene armadillo is highly conserved in sequence and expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polarity protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i-SUBGELLUTAR LOCATION: INNER SURFACE OF CELL MEMBRANE.-i-SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.-i-SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M 10.
73E61F59BDBFA580 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural protein. ASP/GLU-RICH (ACIDIC).
350 CSSNKPAIVEAGGMQALGLHLTDSSQRLVQNCLWTLRNLSD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 191; DB 1;
Pred. No. 6.3e-18;
                                                                                                                 01-JUL-1993 (Rel. 26, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Armadillo segment polarity protein.
                                                                          813 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SWART; SW00185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
Developmental protein; Segmentation Cell adhesion; Cytoskeleton; Structu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARM 3.
ARM 4.
ARM 5.
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-93247062; Pubmed-8483160;
                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.0%;
ilarity 85.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L04874; AAA29292.1; -.
                                                                                                                                                                                 Musca domestica (House fly).
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           813 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         .NFORMATION.
                                                                                                                                                                                                                                          NCBI_TaxID=7370;
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223
265
349
388
430
477
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                                                                                                      01-JUL-1993
01-JUL-1993
                                                                          ARM_MUSDO
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                                                                                        002453;
                                                          ARM_MUSDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.3%; Score 185; DB 1; Length 621; 87.8%; Pred. No. 3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                              Cell adhesion; Cytoskeleton; Structural protein; Repeat.
NOW.TER 1 1 ARM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17CF444607422BAA CRC64;
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2
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0; Mismatches
                                                                                                                                                                                             PIR; S35092; S35092.
HS5P; 002248; IDOW.
MGD; MGI:96650; Jup.
InterPro; IPR000225; Armadillo.
Pfam; PR001544; Armadillo_seq; 11.
SMART; SM00185; ARM; 8
PROSITE; PS50176; ARM_REPEAT; 9.
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ARM 2.
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                                                                                                                                                                     EMBL; M90365; AAB02885.1; -.
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Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          257.
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621 'AA;
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Gaps

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Indels

4; Mismatches

348 CSSNKPAIVDAGGMQALAMHLSNPSPRLVQNCLWTLRNLSD 388

g ò

1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41

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PLAK_HUMAN
           SEQUENCE
 CONFLICT
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                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             laevis.";

Dev. Biol. 153:337-346(1992).

-!- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
OF BOTH THE CYTOSRELETON AND THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOSLOBIN IN BOTH THE DESMOSOMES AND IN THE
INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                        MEDLINE-9309332; PubMed=1459359; Fouquet B., Zimbelmann R., Franke W.W.; Fouquet B., Zimbelmann R., Franke W.W.; "Identification of plakcylobin in cocytes and early embryos of Xenopus laevis: maternal expression of a gene encoding a junctional Differentiation 51:187-194(1992).
                                                                          01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Maphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                                                                                             de Marais A.A., Moon R.T.;
"The armadillo homologs beta-catenin and plakoglobin are
differentially expressed during early development of Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
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ARM 2.
ARM 3.
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ARM 6.
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ARM 9.
ARM 9.
ARM 10.
I -> V (IN REF. 2).
                                              738 AA.
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EMBL, X67078; CAA47463.1; --
PIR; S24636, S24636.
PIR, S35093; S35093.
HSSP, Q02248; 2BCT.
InterPro: IPR000225; Armadillo.
Fam: PF00514; Armadillo.seg; 11.
SMARY; SMO0185; ARM; 10.
PROSITE; PS50176; ARM; REPEAT; 9.
                                            PRT;
                                                                                                                                                                                                                                                                       SEQUENCE OF 133-292 FROM N.A. MEDLINE=93012479; PubMed=1397690;
                                                                01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoskeleton;
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER
                                                                                                                                            Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSOCIATED FORM
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell adhesion;
                                           PLAK_XENLA
P30998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
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                                 PLAK_XENLA
                     RESULT
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                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDIATE 1726765; MEDIATE 18264555; MEDIATE 18264555; MEDIATE 18264555; MEDIATE 18264555; MEDIATE W.M., Goldschmidt M.D., Zimbelmann R., Mueller H.M., Schiller D.L., Cowin P.; Schiller D.L., Cowin P.; Molecular cloning and amino acid sequence of human plakoglobin, the
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PICC. Matl. Acad. Sci. U.S.A. 86:4027-4031(1989)

FICC. Matl. Acad. Sci. U.S.A. 86:4027-4031(1989)

FICC. Matl. Acad. Sci. U.S.A. 86:4027-4031(1989)

FICC. Matl. Acad. Sci. U.S.A. 86:4027-4031(1989)

ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
OF BOTH THE CYTCKELETON AND THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOGLOBIN IN BOTH THE DESWOSOMES AND IN THE
INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; 'Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                     ;
                                                                                                                            Length 738;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR000225: Armadillo.
Pfam; PP00514: Armadillo_seg; 10.
SMART; SM00185; ARM: 8:
PROSITE; PS50176; ARM_REPEAT; 8.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
INIT_MET
            226 :226 A -> T (IN REF. 2).
738 AA; 81711 MW; 569DBE69D08BBC58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                            Query, Match (1785.3%; Score 185; DB 1; L. Best'Local Similarity (87.8%; Pred. No. 3.6e-17; Matches (1786); Mismatches (1797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01:MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       743 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Junction plakoglobin (Desmoplakin III). JUP OR DP3.
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ARM 2.
ARM 4.
ARM 5.
ARM 5.
ARM 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
.226
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252
351
430
473
521
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HSSP; Q02248; 2BCT...
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us-09-641-104a-9.rsp

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
S. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A britton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R.A. Brandon R.C., Rogers Y.-H.C., Balzej R.G., Champe M., Pfeiffer B.D.,
R.A. Brandon R.C., Mascandale J., Bayraktaroquu L., Beasley E.M.,
R.A. Ballew R.M., Basu A., Baxendale J., Bayraktaroquu L., Beasley E.M.,
R.A. Ballew R.M., Buck J., Broketen P., Bolshakov S.,
R.A. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,
R. Burtis K.C., Busam D.A., Danlke C., Davenport L.B., Davies P.,
A Dorkova D., Botchen A., Dong Z., Mays A.D., Dew, I., Dlattz S.M.,
A Hartis K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R.A. Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
R.A. Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R.A. Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mopherson D.,
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89211895; PubMed=2707602; Riggleman B., Wieschaus E., Schedl P.; Molecular analysis of the armadillo locus: uniformly distributed transcripts and a protein with novel internal repeats are associated with a Drosophila segment polarity gene."; Genes Dev. 3:96-113(1989).
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loureiro J., Peifer M.;
"Roles of Armadillo, a Drosophila catenin, during central nervous
GQLA -> DSSL (IN REF. 1; AAA64895).
V -> A (IN REF. 1; AAA64895).
472741F400D388FD CRC64;
                                                                                                                              ó
                                                                                        Length 743;
                                                                          Score 185; DB 1; Lengtn /*.
Pred, No. 3.7e-17;
                                                                                                                                                                                     339 CPSNKPAIVEAGGMQALGKHLTSNSPRLVQNCLWTLRNLSD 379
                                                                                                                                                                  1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
                                                                                                                                                                                                                                                                                             ARM_DROME STANDARD; PRT; 843 AA. P18824; 002371; 09W546; 01-NOV-1990 (Rel. 16, Last sequence update) 01-NOV-1990 (Rel. 16, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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MEDLINE=20196006; PubMed=10731132;
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   99 GC
139 V
81498 MW;
                                                                                             85.3%;
87.8%;
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                                                                                                                                Conservative
   96
139
743 AA;
                                                                                             Query Match
Best Local Similarity
Matches 36; Conserv
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   CONFLICT
CONFLICT
SEQUENCE
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MEDITING-95113174; PUDMAGE-724201;

RT Armadillo: roles for wingless signal and zeste-white 3 kinase.";

Phosphorylation of the Drosophila adherens junction protein

RT Armadillo: roles for wingless signal and zeste-white 3 kinase.";

RT Armadillo: roles for wingless signal and zeste-white 3 kinase.";

Dev. Biol. 166:543-556(1994).

IN THE TRANNARSION OF DEVELOPMENTAL INFORMATION. CAN ASSOCIATE

WITH ALPHA-CATENIN. CYTOPLASMIC ISOFORM ACCUMULATES THROUGH WG

SIGNALING. ARM FUNCTION IN WG SIGNAL TRANSDUCTION IS REQUIRED.

CE SARLY IN DEVELOPMENT FOR DETERMINATION OF NEUROBLAST FATE. ARM AND

ABL PROTEINS FUNCTION COOPERATIVELY AT ADHERENS JUNCTIONS IN BOTH

THE CNS AND BEIDERMIS.

CO SIGNALING. ARM FUNCTION NOW DETERMINATION IN BENDER ALIERMATIVE SPLICING.

ALTERNATIVE PRODUCED: 2 ISOFORMS; CYTOPLASMIC (SHOWN HERE) AND

CO NEURLE, ARE PRODUCED BY ALTERNATIVES SPLICING.

CO NEURLE, ARE PRODUCED BY ALTERNATIVE SPREAMINATE.

CO NEURLE, ARE PRODUCED BY ALTERNATIVE SPREAMINATE.

CO NEURLE, ARE PRODUCED BY ALTERNATIVE SPREAMINAL AND

CO NEURLE, ARE PRODUCED BY ALTERNATIVE OF THE CNS MIDLING.

CO NEURLE, ARE PRODUCED BY ALTERNATIVE OF THE CNS MIDLING.

CO NEURLE, ARE PRODUCED BY ALTERNATIVE OF THE CNS MIDLING.

CO NEURLE, ARE PRODUCED BY ALTERNATIVE OF THE CNS MIDLING.

CO NEURLE, ARE PRODUCED BY ALTERNATIVE OF THE CNS MIDLING.

CO NEURLE, BENDER SA STHEY EXIT THE CNS. BOTH ISOFORMS.

CO NEURLE, BENDER SA STHEY EXIT THE CNS. BOTH ISOFORMS.

CO NEURLE, BENDER SA STHEY EXIT THE CNS. BOTH ISOFORMS.

CO NEURLE, BENDER SA STHEY EXIT THE CNS. BOTH ISOFORMS.

CO NEURLE, BENDER SA STHEY EXIT THE CNS. BOTH ISOFORMS.

CO NEURLE, BENDER SA STHEY EXIT THE CNS. BOTH ISOFORMS.

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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount, S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nalson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Palazolo M., Pittman G.S., Pan S., Scheeler F., Shen H.,
RA Palazolo M., Stennogton K., Saunders R.D.C., Scheeler F., Shen H.,
RA Palazolo M., Stennog R., Shen H.,
Rapier E., Stenington K., Standers R.D.C., Scheeler F., Shen H.,
Rapier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Rapier E., Parazining A.C., Stapleton M., Strong R., Sun E.,
Rapier E., Parazining A.C., Stapleton M., Strong R., Wang X.,
Rapier E., Parazining A.C., Turner R., Venter E., Wang A.H., Wang X.,
Rapier E., Parazining R., Melnstock G.M., Welssenbach J.,
Rapier E., Parazining R., Lander M., Zhong W., Zhou K., Zhao Q.A.,
Rapier E., Myers E.W., Rubin G.M., Venter J.C.;
R Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
R Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
R Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIATE CALL OF STATES TO MAIN THE STATES D., MEDIATES D., MEDIATES D., Gatt M.K., Ashburner M., Murphy L., Harris D., Menos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E., Barrell B.G., Ferraz C., Vidal S., Brun C., Demailies J., Cadieu E., Dragano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Modolell M., Dowe G., Schoettler P., Werner M., Mourkioti F., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Modillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM). STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95113174; PubMed=7529201;
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APHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
PROPERN WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
TSEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE BETA-CAT SIMILARITY: CONTAINS 7 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-93305730; Pubmed-8318544;
Rosenthal E.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01; FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                  89361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 34; Conserve
                                                                                                                                                                                                                                                                                                                                                820 AA;
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SEÇUENCE
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P35224;
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REPEAT
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REPEAT
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Matches
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   entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               ARM 13 (INCOMPLETE).

ASP/GLU-RTCH (AGIDIC).

LGPERATEGLYGOGPPSVHSSHGGRAFHOOGYDTLFIDSMO
GLEISSPVGGGAGGAGGAPGGAVGGASGGGGNIGAIPPSGA
BYEFYSKDMUNDVGEIDAGALNFDLDAMFTPPNDNNNLAAWYD
TDC -> ILYQ (IN NEURAL ISOFORM).

40DADGFBB3163049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tripneustes gratilla (Hawaian sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of homologues to beta-catenin/plakoglobin/armadillo in two invertebrates, Urechis caupo and Tripneustes gratilla."; Biochim. Biophys. Acta 1173:337-341(1993).
                                                                                                                                                                       PROSITE; PS50176; ARM_REPEAT; 9.
PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Phosphorylation; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 179; DB 1; Length 843;
Pred. No. 2.7e-16;
3; Mismatches 4; Indels
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01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   820 AA
                                        AF001213; AAB58731.1; --
AE003422; AAF45688.1; ALT_INIT.
AL021106; CAA15946.1; --
AL021086; CAA15946.1; JOINED.
AL021086; CAA15935.1; --
AL021106; CAA15935.1; JOINED.
                                                                                                                                                                                                                                                                                              ARM 8.
ARM 9.
ARM 10.
ARM 11.
ARM 12.
ARM 13
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                                                                                                                                         InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-93305730; PubMed-8318544;
                                                                                                                                                                                                                          ARM
ARM
ARM
ARM
ARM
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01-FEB-1994 (Rel. 28, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                          91152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.5%;
Best Local Similarity 82.9%;
Matches 34; Conservative 3
                                EMBL; X54468; CAA38350.1; -.
                                                                                                                                 FlyBase; FBgn0000117; arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                   , A31861.
                                                                                                                                                                                                                                                                                                                                                                                                          843 AA;
                                                                                                              Q02248; 1DOW.
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                                                                                                                                                                                                                                            243
285
327
369
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533
585
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648
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                                                                                                                        RANSFAC; T0297
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                                                                                                     PIR; A31861
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P35223;
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VARSPLIC
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-IT FUNCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL

ADHESTON MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MENBRANE)

-TOTELINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A

COMPLEX WHICH IS LINED TO THE ACTIN FILAMENT NETWORK, AND WHICH

SEEMS TO BE OF:PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of homologues to beta-catenin/plakoglobin/armadillo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in two invertebrates, Urechis caupo and Tripneustes gratilla.";
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Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57255E0F57795FD3 CRC64;
THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.1%; Score 176; DB 1; L4
82.9%; Pred. No. 6.6e-16;
vative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSD 41
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01-MAR-2002 (Rel. 41, Last annotation update)
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ARM 2.
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ARM 5.
ARM 6.
ARM 7.
ARM 8.
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apparently multiple nuclear functions including the

participates in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
10-JUL-1993 (Secine-rich RNA)
10-JUL-1993 (Secine-rich RNA)
10-JUL-1993 (Secine-rich RNA)
10-JUL-1993 (Rel. 1993)
10-JUL-1993 (Rel. 1
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"Yeast Srpl, a nuclear protein related to Drosophila and mouse pendulin, is required for normal migration, division, and integrity of nuclei during mitosis.";
Mol. Gen. Genet. 248:351-363(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94316601; PubMed-8041713;
Yano R., Oakes M.L., Tabb M.M., Nomura M.;
"Yeast Srpip has homology to armadillo/plakoglobin/beta-catenin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 818;
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Obermaier B., Piravandi E., Rinke M., Domdey H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1DF174BEEF745C1D CRC64;
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ARM 2.
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                                                                                                                                                                                                                                                                        InterPro: IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
BARAT; SM00185; ARM; ILP.
PROSTITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89070 MW;
                                                                                                                                                                                                                           EMBL; L10355; AAA30330.1; -.
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Matches 30; Conservative
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495
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501
543
648
818 AA;
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002821;
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                                                                                                                                                                                                                                                                         X-RAY:CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 89-510.
MEDLINE=98359119; PubMed=9695948;
Gorti 1s., Uy M., Leighton L., Blobel G., Kuriyan J.;
Crystallographic analysis of the recognition of a nuclear localization signal by the nuclear import factor karyopherin alpha.";
Cell 94:193-204(1998).
194:193-204(1998).
ETHER A SIMPLE OR BIPARTITE NLS MOTIF. PROMOTES DOCKING OF IMPORT SUBSTRATES. TO THE NUCLEAR ENVELOPE. SEEMS TO ACT AS A CYTOSOLIC RECEPTOR FOR BOTH.SIMPLE AND BIPARTITE NLS MOTIFS (BY SIMILARITY).
-:- SUBUNIT: FORMS A COMPLEX WITH AN IMPORTIN BETA SUBUNIT. INTERACTS
WITH CSEL.
                                                                                                                                                                                                                              involving transport substrate, transport factors, and nucleoporins."; Cell 83:683-692(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARM 1.
ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 7.
ARM 8.
ASP/GLO-RICH (ACIDIC).
S->F: IN SRP1-31; TS MUTANT; REDUCED GROWTH RATE AND CHROMOSOME LOSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; 3D-structure,
                                                                                                                                                              NUCLEOPORIN REPEAT BINDING REQUIREMENT.
MEDLINE=96097112; PubMed=8521485;
Rexach M., Blobel G.;
"Protein import into nuclei: association and dissociation reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . NUCLEUS.

-1-MISCELLANEOUS: BINDS TO NUCLEOPORIN FXFG BUT NOT GLEG REPEAT
REGIONS. RAN-GTP CAN DISRUPT THE KARYOPHERIN HETERODIMER BY
BINDING TO THE BETA SUBUNIT AND RELEASES BOTH SUBUNITS FROM THE
DOCKING SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITH CSEI.
-1- SUBCELLULAR LOCATION: MAINLY LOCALIZED AT THE PERIPHERY OF THE
                                                              MEDLINE-95348058; PubMed-7622450;
Enenkel C., Blobel G., Rexach M.;
"Identification of a yeast karyopherin heterodimer that targets
import substrate to mammalian nuclear pore complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1: SIMILARITY: BELONGS TO THE IMPORTIN ALPHA FAMILY.
             maintenance of the nucleolar structure.";
Proc. Natl. Acad. Sci. U.S.A. 91:6880-6884(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfani, PPF0514 Armadillo_seg; 8.
Pfani, PPF0149; IBB; 1.
SMART; SM00185; ARM; 8.
PROSITE; PSS0176; ARM; REPEAT; 2.
Transport; Protein transport; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M75849; AAA35090.1; -. EMBL; Z71465; CAA96083.1; -. PIN; S30884, S30884. PDBS; 1BK5; 16-FBB-99. PDB; 1BK6; 13-JAN-99.
                                            [5] . . IDENTIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEUS.
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MUTAGEN
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Nan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Buck J., Brckstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadjeu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K.J., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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Eukaryota; Wetazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophillade; Drosophila.
E->K: IN SRP1-49; TS MUTANT; ALTERATION IN NUCLEOLAR AND MICROTUBULE MORPHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                P->0: IN SRP1-1; TS MUTANT.
D->N: IN SRP1-3; TS MUTANT.
E->K: IN SRP1-2; TS MUTANT.
G->V: IN SRP1-54; TS MUTANT; REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Pendulin, a Drosophila protein with cell cycle-dependent nuclear localization, is required for normal cell proliferation."; J. Cell Biol. 129:1491-1507(1995).
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J. Cell Biol. 129:1473-1489(1995).
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PS2255; Q2443; Q9V445;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
IMPOCTION (Rel. 40, Last annotation update)
PEN OR OHO31 OR CG4799.
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                                                                                                                                                                                                                                                                                                                                         28.1%; Score 61; DB 1; Length 542; 30.3%; Pred. No. 1.2; 1.1ve 10; Mismatches 13; Indels
                                                                                                                                                                                                                                         8D3A0CB76F2E7C00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 VINAGVLPALRILLSSPKENIKKEACWTISNIT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 IVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLS 40
                                                                                                                                                                                                            GROWTH RATE
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MEDLINE=95310331; Pubmed=7790350;
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                                                                                                                                                                                                                                         60441 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                         542 AA;
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                                                                    219
286
360
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Adali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,
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Science 289:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: BINDS SPECIFICALLY AND DIRECTLY TO SUBSTRATES CONTAINING EITHER A SIMPLE OR BIPARTITE NLS MOTIF. PROMOTES DOCKING OF IMPORT SUBSTRATES TO THE NUCLEAR ENVELOPE. SEEMS TO ACT AS A CYTOSOLIC. RECEPTOR FOR BOTH SIMPLE AND BIPARTITE NLS MOTIFS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: FORMS A COMPLEX WITH IMPORTIN BETA SUBUNIT.
SUBCELLULAR LOCATION: SHUTTLES BETWEEN THE CYTOPLASMIC AND NUCLEUS
IN A CELL CYCLE-DEPENDENT MANNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HALF OF EMBRYOGENESIS REACHING A MAXIMUM BETWEEN. 4 AND 8 HRS OF DEVELOPMENT. PROTEIN EXPRESSION INVERASES AGAIN FROM THE THIRD LARVAL INSTAR ONWARDS. IT IS EXPRESSED IN A MATERNAL/EARLY EMBRYOUIC PHASE, AND AGAIN DURING MORPHOGENESIS IN LATE LARVAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE NEUROBLAST STEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERVE AS AN ADAPTER MOLECULE TO FORM COMPLEXES WITH OTHER PROTEINS. MAY ACT AS A TUNOR SUPPRESSOR IN HEMATOPOLETIC CELLS. MAY PLAY A ROLE IN THE NUCLEAR IMPORT OF KARYOPHILIC PROTEINS AND SOME OF THESE MAY BE REQUIRED FOR THE NORMAL TRANSMISSION AND FUNCTION OF PROLIFERATIVE SIGNALS IN THE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: HIGH LEVELS ARE DETECTED DURING THE FIRST
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--- SIMILARITY: BELONGS TO THE IMPORTIN ALPHA FAMILY.
--- SIMILARITY: CONTAINS 10 ARM REPEATS.
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Pfam; PF01749; IBB; 1.
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PROSITE; PS50176; ARM_REPEAT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000225; Armadillo.
InterPro; IPR002652; IBB.
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HSSP; Q02821; 1BK5.
Flydaše; FBgn0011823; Pen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altered coding sequence of the pedigree.";
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       "A novel moesin-, ezrin-, radixin-like gene is a candidate for the neurofibromatosis 2 tumor suppressor.";
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                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
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                                                                                   Length 522;
ARM 8.
ARM 9.
ARM 10.
ASP/GLU-RICH (ACIDIC).
L -> P (IN REF. 1).
v; B02773EB76812AD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99036680; PubMed-9817927;
Zucman-Rossi J., Legoix P., Der Sarjussian H., Cheret G.
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"NF2 gene in neurofibromatosis type 2 patients.";
Hum. Mol. Genet. 7:2095-2101(1998).
                                                                                                        14;
                                                                                    DB 1;
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U
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16-OCT-2001 (Rel. 40, Last annotation update)
Merlin (Schwannomin) (Neurofibromin 2)
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                                                                                    Score 60; DB:
Pred. No. 1.6;
9; Mismatches
                                                                                                                                                                                                      595 AA
                                                                                                                                            320 VIASGGLPRLGLLLQHNKSNIVKEAAWTVSNIT 352
                                                                                                                              8 IVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLS 40
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"DNA diagnosis of neurofibromatosis 2.
merlin tumor suppressor in an extended
JAMA 270:2316-2320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=93201601; Pubmed=8453669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT NF2 TYR-220.
MEDLINE-94047514; PubMed-8230593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-93281181; Pubmed-8379998;
                                                                                                        9;
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                                           69 I
57821 MW;
                                                                                    27.6%;
30.3%;
                                                                                                         Conservative
                                                                                                                                                                                                       STANDARD;
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VARIANT NF2 PHE-96 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 72:791-800(1993).
                                                                                                                                                                                                      MERL_HUMAN STANDAI
P35240; 095683;
01-FEB-1994 (Rel. 28,
01-FEB-1994 (Rel. 28,
                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                      522 AA;
                                                                                               Best Local Similarity
                                                                                                         10;
                                                                                                                                                                                                                                                                    NF2 OR SCH.
                    REPEAT
DOMAIN
CONFLICT
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  REPEAT
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MEDLINE-95038740; PubMed-7951231; Sainz J., Huynh D.P., Figueroa K., Ragge N.K., Baser M.E., Pulst S.M.; Sainz J., Huynh D.P., Figueroa K., Ragge N.K., Baser M.E., Pulst S.M.; "Mutations of the neurofibromatosis type 2 gene and lack of the gene product in vestibular schwannomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94214500; PubMed-8162073; Blanchi A.B., Hara T., Ramesh V., Gao J., Klein Szanto A.J., Morin F., Menon A.G., Trofatter J.A., Gusella J.F., Seizinger B.R., Kley N.; "Mutations in transcript isoforms of the neurofibromatosis 2 gene in
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MEDLINE-9436282; Bubmed-80811368;
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"Gerniine mutations in the neurofibromatosis type 2 tumour suppressor
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Baserim.E., Kluwe L., Mautner V.-F.;
"Germ-line NF2, mutations and disease severity in neurofibromatosis
type 2 patients with retinal abnormalities.";
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                                                                                                                                                                                                                                                                                                                                   Barton D.E., Xuereb J.H.,
MEDITRE-94311312; PubMed-7913580;
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MEDLINE-94282032; bubMed-8012353;
Jacoby L.B., Maccollin M., Louis D.N., Mohney T., Rubio M.P.,
Pulaski K., Trofatter J.A., Kley N., Selzinger B., Ramesh V.,
Gusëlla J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the NF2 gene in schwannomas.";
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                                                                                                                                                                                                                                                                                WARIANT ARG-46:
MEDLINE-94272478; PubMed-8004107;
Irving R.M., Moffat D.A., Hardy D.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       schwannoma."; ; ; ; Hum; Mol. Genet. 3:347-350(1994).
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Hum: Mol. Genet. 3:413-419(1994)
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Nat. Genet. 6:185-192(1994).
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Hum. Genet. 97:632-637(1996).
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MEDLINE-94272478; Pu
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Ramesh V.
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                                                     AND OVARY.

-I DISEASE: NEUROFIEROMATOSIS 2 (NF2) OR CENTRAL NEUROFIEROMATOSIS IS
A GENETIC DISORDER CHRARCTERIZED BY BILATERAL VESTIBULAR
SCHWANNOMAS (FORMERLY CALLED ACOUSTIC NEUROMAS), SCHWANNOMAS OF
OTHER CRANTAL AND PERPHERAL NERVES, MENINGTOMAS, AND EPENDYMONAS.
IT IS INHERITED IN AN AUTOSOMAL DOMINANT FASHION WITH FULL
PENETRANCE. AFFECTED INDIVIDUALLS GENERALLY DEVELOP SYMPTOMS OF
EIGHTH-NERVE DYSEUDOTION IN EARLY ADULTHOOD, INCLUDING DEFENESS
AND BALANCE DISORDER. ALTHOUGH THE TUMORS OF NF2 ARE
HISTOLOGICALLY BENIGAN, THEIR ANATOMIC LOCATION MAKES MANAGEMENT
DIFFICULT, AND PATIENTS SUFFER GREAT MORBIDITY AND MORTALITY.
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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LYVYMLXVVMVLPSVILTRA (IN ISOFORM 2).
L-> R (IN VESTIBULAR SCHWANNOMA).
/FTId=VAR_000809.
F -> S (IN NF2).
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PROSITE; PS00661; BAND_41_2; 1.
PROSITE; PS50057; BAND_41_3; 1.
Structural protein; Cytoskeleton; Anti-oncogene; Disease mutation;
Am. J. Hum. Genet. 64:1230-1233(1999).
-!- FUNCTION: PROBABLY ACTS AS A MEMBRANE STABILIZING PROTEIN.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
                                  PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=vAR_000810.
K -> G (IN VESTIBULAR SCHWANNOMA).
/FTId=vAR_000811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN NF2 AND SPORADIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_000812.
E -> G (IN NF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTIG=VAR_000813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.1-LIKE,
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                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X72665; CAA51220.1; JG
EMBL; X72666; CAA51220.1; JG
EMBL; X72667; CAA51220.1; JG
EMBL; X72669; CAA51220.1; JG
EMBL; X72669; CAA51220.1; JG
EMBL; X72669; CAA51220.1; JG
EMBL; X72670; CAA51220.1; JG
EMBL; Z22664; CAA80377.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y18000; CAA76992.1;
EMBL; Y18000; CAA76993.1;
PIR; S33809; S33809.
                                                                                                                                                                                                                                                                                                              EMBL; X72655; CAA51220.1;
EMBL; X72656; CAA51220.1;
EMBL; X72657; CAA51220.1;
                                                                                                                                                                                                                                                                                                     EMBL; L11353; AAA36212.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00373; Band_41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                               EMBL; X72658; CAA51220.1
EMBL; X72659; CAA51220.1
EMBL; X72660; CAA51220.1
EMBL; X72661; CAA51220.1
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X72663; CAA51220.1
EMBL; X72664; CAA51220.1
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SMART; SM00295; B41; 1.
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595
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain; MEDLINE-9507270; Pubmed-7981675; M.; MEDLINE-95072570; Public S.M.; Huynh'b.D. , Nechiporuk T., Pulst S.M.; Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are conserved and code for schwannomins with distinct C-terminal domains.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haase V.H., Trofatter J.A., Maccollin M., Tarttelin E., Gusella J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The murine NF2 homologue encodes a highly conserved merlin protein with alternative forms."; Hum: Mol. Genet. 3:407-411(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claudio J.O., Marineau C., Rouleau G.A.;
"The mouse neurofibromatosis type 2 gene maps to chromosome 11.";
Genomics 21:437-439(1994).
                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1-FUNCTION: PROBABLY ACTS AS A MEMBRANE STABILIZING PROTEIN.
-1-ATTERNATIVE PRODUCEY: AT LEAST 3 ISOFORMS ARE PRODUCED BY ALTERNATIVE SELLCING.
-1-SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
      Length 595;
                                                                Indels
                                                             10;
DB 1;
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOY-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Merlin (Schwannomin) (Neurofibromin 2).
Mus musculus (Mouse).
      Score 59.5; D
Pred. No. 2.1;
                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGB; MGI:97307; MEZ.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; Ezrin_radixin_moesin.
Pfäm;(PF00373; Band_41: 1
                                                                                                                                                      235 GVDALGLHYDPENRLTPKISFPWNEIRNIS 265
                                                                                                                    13 GMQALGLHLTDPSQRLYQNCL--WT-LRNLS 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-94282031; Pubmed-8012352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94375073; PubMed-8088840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 400-596 FROM N.A.
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EMBL; L27009; AAA63848.1; --
EMBL; L28176; AAA39808.1; --
EMBL; X75759; CAA53386.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; (X74671; CAA52737.1; -.
   Ouery/Maich
Best Local Similarity, 45.2%,
Matches: 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, ('PF00373, Band 41; 1.
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00935; BAND41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI-TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                              MERL: MOUSE
P46662;
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DR PROSITE; PS00661; BAND_41_2; 1.

DR PROSITE; PS50057; BAND_41_3; 1.

KW Structural protein; Cytoskeleton; Anti-oncogene; Alternative splicing.

FT DOMAIN 74 241 BAND 4.1-LIKE.

FT VARSPLIC 581 S96 SECOND ISOFORM).

FT CONFLICT 475 475 I --7 (IN REF. 2).

FT CONFLICT 554 54 A -> R (IN REF. 2).

FT CONFLICT 570 570 G -> A (IN REF. 2).

SQ SEQUENCE 596 AA; 69691 WW; 8D06E3B07D2C5851 CRC64;
```

 Query Match
 27.4%;
 Score 59.5;
 DB 1;
 Length 596;

 Best Local Similarity 45.2%;
 Pred. No. 2.1;
 Matches 14;
 Conservative 4;
 Mismatches 10;
 Indels 3;
 Gaps

 Qy 13 GMOALGHITDPRORIZORIZOROL-TRINLS 40
:			;	
:			;	
:		;		
 Db 235 GVDALGHITDPENRITPRISFPWNEIRNIS 265

; ;

Search completed: July 29, 2002, 16:09:54 Job time: 759 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 29, 2002, 16:07:55; Search time 158.47 Seconds Run on:

(without alignments)
27.336 Million cell updates/sec

US-09-641-104A-10 Title: Perfect score:

1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

747574 segs, 111073796 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_032802:*

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
22: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,												
Description		Human beta-catenin	Human beta-catenin	Human beta catenin	Human beta-catenin	Novel human secret	Human beta-catenin	Mouse beta-catenin	Novel human secret	Drosophila melanod	Drosophila melanog	Drosophila melanog
ID		AAY33221	AAY33236	AAB07290	AAY70740	AAU28118	AAE06038	AAE06039	AAU28306	ABB60196	ABB65819	ABB65821
DB	;	20	20	21	21	22	22	22	22	22	22	22
Ouery Match Length DB ID		39	38	781	781	781	781	781	800	840	840	840
Query Match I		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	79.9	79.9	79.9
Score		194	194	194	194	194	194	194	194	155	155	155
Result No.		1	7	æ	4	ഗ	9	7	80	თ	10	11

Cellular Receptor	Drosophila melanog	Drosophila melanog	Ü		13	Arabidopsis thalia	Novel human secret	LXXLL sequence for	Arabidopsis thalia	ß	Drosophila melanog	C. glutamicum pfkA	Corynebacterium gl	C glutamicum prote	Streptococcus pneu	Drosophila melanog	Alpha subunit of A	Flea saliva protei	Ø	Amino acid sequenc	Amino acid sequenc	Mastadenovirus 45	Protoporphyrinogen	Amino acid sequenc	Amino acid sequenc	Drosophila melanog	Staphylococcus aur	Staphylococcus aur	Amino acid sequenc	sed	lrus	Human host cell pr	Human host cell pr
AAR11354	ABB64252			AAG31301	AAG31300																		AAW73956			ABB6944	AAU33897	AAU3670	AAY6864	AAB3173	AAB67	AAW1632	AAB70386
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128	ß	. 55	. 22	5	54	24	.: 5	'n.	. 52		25	ч	$\overline{}$	$\overline{}$	51.5	⊣	\vdash	. 21	51	51	21	. 51	51	0	50.5	0	20	. 20	20	50	20	20	20
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ALIGNMENTS

AAY33221 RESULT

AA. AAY33221 standard; peptide; 39

AAY33221;

(first entry) 18-NOV-1999 Human beta-catenin protein armadillo repeat arm7 fragment.

modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor superessor gene; conductin; E-cadherin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth. Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; THE STATE OF THE S

Homo sapiens.

DE19909251-A1.

26-AUG-1999.

99DE-1009251. 22-FEB-1999; 98DE-1007390 21-FEB-1998; (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

Von Kries J; Birchmeier W,

WPI; 1999-470389/40.

Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor

Example 4; Fig 5; 116pp; German.

suppressor gene products

suppressor gene products

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Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor
                                                                                                                                                                                                                                                                                                                                                                                                  (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                             AAY33236 standard; peptide; 39 AA
           Disclosure; Page 7; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                       98DE-1007390
                                                                                                                                                                                                                                                                                                                                                                            99DE-1009251
                                                                                                                                                                                                                                                                                                                                                                                                               Birchmeier W, Von Kries J;
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          NPI; 1999-470389/40.
                                                                                                                                                           39 AA;
                                                                                                                                                                                                                                                                                                                                                    DE19909251-A1.
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                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1999;
                                                                                                                                                                                                                                                                      18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                               26-AUG-1999
                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                               invention
                                                                                                                                                                                                                                                          AAY33236;
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                  Homo
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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beth catenin with transcription factors or products of tumor suppressor genes, The invention also describes (a) peptides (II) comprising part of the invention also describes (a) peptides (II) comprising part of the invention and related molecules (III) from the armadillo domain (arm units) (b) peptides and related molecules (III) from the complete beta-catenin molecule, that include at least one of the specific interaction domains for LBF-1, TCF-4, APC, conductin or complete beta-catenin molecule, that include at least one of the specific interaction domains for LBF-1, TCF-4, APC, conductin or screening substance linked immunosorbent assay (ELISA) for correction with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin is a key compound in the wint signalling pathway and is involved in development of funors. Generally its interaction with LEF-1 or TCF-4 is oncogenic. (A) which inhibit interaction are particularly used to treat tumors, especially carcinome of the colon and melanome, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically mair growth. AAY33230-Y33241 represent mutant the method of the colon in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.

Best Local Similarity 100.

Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta catenin; çadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-410651/35::-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 ÀA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; colorec
gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB07290;
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which is based on substances (I) that modulate (inhibit or promote) the which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides (I) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the complete beta-catenin molecule, that include at least one of the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or Screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin is the Wint signalling pathway and is involved in development of tumors. Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is oncogenic. (A) which inhibit interaction mare particularly used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; B-cadharin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treat tumors, especially carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth. AAY32217 '733222 represent human beta-catenin armadillo repeat fragments described in the method of the
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4.7e-21;
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compounds targeting nucleic acids encoding human beta catenin (HBC) useful for treating diseases associated with HBC expression and as prophylaxis to prevent or delay infection, inflammation or tumor formation
                                                                                                                                                                                                             atenin; cadherin; metastasis; cadherin-associated protein; colorectal cancer; melanoma; antisense oligonucleotide;
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 Length 39;
                       Indels
100.0%; Score 194; DB 20;
100.0%; Pred. No. 4.7e-21;
iive 0; Mismatches 0;
                                          1 AATKOEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                         AAB07290 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                              :99US-0344519.
                                                                                                                                                                                                                                                                                                                                                  25-JUN-1999; . 99US-0344519
                                                                                                                                                                      01-NOV-2000 (first:entry)
                                                                                                                                                                                                                                                                                                                                                                                               Cowsert LM;
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Human beta-catenin; Wnt antagonist; contraceptive; contraceptive vaccine; oocyte development; female primate contraception; oocyte viability; monoclonal antibody; Wnt signalling.
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                                                   Beta catenin is a member of the catenin family of cytosolic proteins and a key member of the Mat signalling pathway. Catenins interact with the cytoplasmic domains of cadherin glycoproteins, and are important in maintaining cell adhesiveness. The loss of cell adhesiveness is implicated in metastasis. Beta catenin is also known as cadherin-associated protein and is implicated in colorectal cancer and melanoma. The present sequence is the human beta catenin protein. The coding sequence of this protein was used in the present invention to design antisense oligonuclectides (AAA58327-A58366). The oligonuclectides are capable of hybridising to human beta catenin, in order to inhibit expression of human beta catenin. The oligonuclectides may be used in gene therapy for colorectal cancer or melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contraceptive composition for inhibiting oocyte development in a female primate comprises a Wnt polypeptide antagonist
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                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 194; DB 21;
100.0%; Pred. No. 1.6e-19;
ive 0; Mismatches 0;
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                   Columns 45-52; 35pp; English,
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Best Local Similarity 100.0
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200021555-A1
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               Example 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency, SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
or more armidillo-like repeats which participate in cadherin binding. Other, mutants include those lacking amino acids 555-781 or 424-781, or 1-422 of beta-catenin.
                                                                                                                                                                                    Gaps
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Wang J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders
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                                                                                                                                              Length 781;
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                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                         391 aatkqegmegllgtlvqllgsddinvvtcaagilsnltc 429
                                                                                                                                                                                                             1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                              1.6e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human secretory protein, Seq ID No 287.
                                                                                                                                            100.0%; Score 194; DB
                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                           AAU28118 standard; Protein; 781 AA
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2000US-0596193.
2000US-0616847.
2000US-0665363.
                                                                                                                                                                  Best Local Similarity, 100.0%;
Matches 39; Conservative
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17-JUN-2000; 2000US-0556193
14-JUL-2000; 2000US-0516847
19-SEP-2000; 2000US-0665363
20-OCT-2000; 2000US-0693267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-2001; 2001WO-US04942
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                Best Local Similarity
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                             AAU28118;
                                                                                              Sequence
                                                                                                                                                 Query Match
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Disclosure; Page 23-24; 33pp; English.

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coring and for regeneration of bone, cartilage, tendon, ligament and/or nerve and for regeneration of bone, cartilage, tendon, ligament and/or nerve clasue growth, and in tissue repair, healing of burns, incisions, clasue growth, and in tissue repair, healing of burns, incisions, clasue growth, and in tissue repair, healing of burns, incisions, clasue growth, and in tissue repair, healing of burns, incisions, clasue growth, and in tissue repair, healing of burns, incisions, conference of gisorders, or periodontal disease. Furthermore, (I) is also useful for cut protection or regeneration and treatment of lung or liver fibrosis, creperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or cupantial infections, autofinmune disorders e.g. multiple sclerosis, crhematoid arthritis, diabetes mellitus, myasthenia gravis, altergic reactions and conditions, such as asthma or other respiratory problems. Cf ertility, metabolism, catabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides catuvity and can act as an antigen in a vaccine composition to raise an entigen metaponer in the composition to raise an entigen and composition to raise and the composition are created protein
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the polypeptide as well as for studying modulators of the polypeptides.

(I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoletic function; allogeneic recipient; signalling pathway; beta-catenin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 194; DB 22; 100.0%; Pred. No. 1.6e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01459.
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Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 AA;
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mammalian stem, or progenitor cells, which comprising increasing the mammalian stem, or progenitor cells, which comprising increasing the increasing the increasing the increasing the concentration of beta-catenin in a progenitor or stem cell in an invitor outlive medium for a period sufficient for the progenitor or stem cell to divide. The number of cells having the functional sphenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoletic function to autologous or alloquence recipients. The present sequence is human beta catenin protein. Beta-catenin is a pivotal player in the signalling pathway intilated by Wnt proteins, which are mediators of several developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 aatkqegmegllgtlvqllgsddlnvvtcaagilsnltc 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse beta-catenin protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-465328/50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD11165.
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best; Local Similarity
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                                                                                                                                                                                                                                                                                                                                         processes.
                                                                                                                                                                                                                                                                                                                                                                            Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE06039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The invention relates to novel isolated human secreted polypeptides (I)

Example 2; SEQ'ID:No 663; 107pp; English.

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in an in vitro culture medium for a period sufficient for the progenitor or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their puluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoietic function to autologous or allogeneic recipients. The present sequence is mouse beta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway initiated by Wnt proteins, which are mediators of several developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 781 AA;
                                                                                                                                                                                                                                                                                                                                                                            processes.
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Gaps
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 Length 781;
                                Indels
100.0%; Score 194; DB 22;
100.0%; Pred. No. 1.6e-19;
ive 0; Mismatches 0;
                                                                              391 aatkqegmegllgtlvqllgsddinvvtcaagilsnltc 429
                                                             1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                Conservative
                 Best Local Similarity
                               39;
 Query Match
                               Matches
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RESULT

AAU28306 standard; Protein; 800 AA 18-DEC-2001 (first entry) AAU28306; AAU28306

Novel human secretory protein, Seq ID No 663.

ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral alzheimer's platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; althery; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; fertility; analgesic; pain; antigen.

Homo sapiens.

WO200166689-A2.

05-MAR-2001; 2001WO-US04942

13-SEP-2001

2000US-0574454. 2000US-0596193. 2000US-0519705 07-MAR-2000; 19-MAY-2000; 17-JUN-2000;

2000US-0616847. 2000US-0665363.

14-JUL-2000; 19-SEP-2000; 20-0CT-2000;

2000US-0693267

Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster

pharmaceutical.

WO200171042-A2.

27-SEP-2001.

Drosophila melanogaster polypeptide SEQ ID NO 7380.

26-MAR-2002 (first entry)

ABB60196;

ABB60196 standard; Protein; 840 AA.

σ

RESULT

(HYSE-) HYSEQ INC.

Ma Y, Zhou P; AJ, Wang J; Wehrman T, Ren F, ng J, Chen R, Xue Asundi V, Xu C, Wehrm Drmanac RT, Zhang J, Liu C, A Yang Y, Zhao QA, rang YT,

WPI; 2001-589934/66. N-PSDB; AAS45206.

Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -

23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150. 23-MAR-2001; 2001WO-US09231

(PEKE;) PE CORP NY

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and polynucleotides (II). (I) and (III) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing hematopolesis, stem cell survival, bone growth and, remodeling (I), (II) and modulators of (II) are useful for reacting transgenic animals useful for studying the in vivo activities of creating transgenic animals useful for studying the in vivo activities of the polypeptides.

(I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and can brain tissue and is useful for the treatment of central and can brain stayled diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral cativity, regulation of haematopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartillage, tendon, ligament and/or nerve of the contral and of bone, cartillage, tendon, ligament and/or nerve of the contral and of bone, cartillage, tendon, ligament and/or nerve of the contral and of bone, cartillage, tendon, ligament and/or nerve of the contral and of bone, cartillage, tendon, ligament and/or nerve of the contral and of bone, cartillage, tendon, ligament and/or nerve of the contral contral that and in these repair, healing of burns, incisions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity
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(ABB57137-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000 or more and cell-cell
                                                                               solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection reagent for detecting 1000 for elucidating cell signalling and c
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                                                                                                                                  ID NO 7380; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                 Length 840;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 24249.
                                                                                                                                                                                                                                                                                                                                                                                                                                      396 aatkvegleallqslvqvlgstdvnvvtcaagilsnltc 434
                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                    Score 155; DB 22;
Pred. No. 8.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                         1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΕŇ
              Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers
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              Li PWD,
                                                                                                                                                                                                                                                                                                                                                                  79.98;
79.58;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 79.58
Matches 31, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
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              Adams M,
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                                       WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                             840 AA;
                                                                                                                                   SEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL09922
                                                    N-PSDB; ABL04299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                          interactions
                                                                               isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila;
            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB65819
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                               genes
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Disclosure; SEQ ID NO 24249; 21pp + Sequence Listing; English.

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                                                                                                         sequences (ABL01840-ABL16175) and the encoded proteins (ARB7377-ABR2072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at frp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell. interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 24255; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                           Length 840;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 24255.
                                                                                                                                                                                                                                                                                                                                                    396 aatkvegleallgslvqvlgstdvnvvtcaagilsnltc 434
                                                                                                                                                                                                                                                                                                                                1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                               Score 155; DB 22;
Pred. No. 8.1e-14;
                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD,
                                                                                                                                                                                                                                                               79.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first.entry)
                                                                                                                                                                                                                                                                                                   Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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11:JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB65821;
                                                                                                                                                                                                                Sequence
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Gaps

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Indels

Length 700;

Score 128; DB 12; Pred. No. 5.5e-10;

Pred. No. 5.564; Mismatches

developmental biology; cell signalling; insecticide;

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Drosophila melanogaster polypeptide SEQ ID NO 19548.
                                                                                                2 ATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                             ABB64252 standard; Protein; 228
                      Best Local Similarity 65.8%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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N-PSDB; ABL08355.
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                                                                                                                                                                                                                                                                                                      pharmaceutical
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                                                                                                                                                                                                                                                                                         Drosophila;
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The ligand pref. includes a fragment indicated in the features, or the total protein. The ligand pref. contains only a single BS and has an amino acid sequence <100 (pref. <20) residues in length. The ligand may also comprise a plurality of fragment 389.394. A therapeutic compsn. contg. the polypeptide is used to stimulate or inhibit B lymphocyte proliferation in patients with B cell lymphona. B lymphocytes and myeloma's can be stimulated in patients with immunodeficiencies and immunoglobulin secretion by hybridoma cultures can be boosted. The compsn. can be administered to inhibit infection in vitro or in
                                                                                                                                                                                                                                                                                                   Cellular receptor 2; CR2; binding site; BS; auto-immune disease; Epstein-Barr Virus; EBV; B lymphocyte; ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to
                                                                   ;
                                      Length 840;
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA segment encoding CR-2 ligand and CR2 binding site treat auto-immune disease, B-cell lymphoma and inhibit Epstein-Barr virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                         385..400
/note= "fragment pref. inlcuded"
389..394
/note= "fragment most pref. included"
                                                                                                           "fragment pref. included"
                                                                                           1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                        Score 155; DB 22;
Pred. No. 8.1e-14;
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           ..309
--- "fragment most
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                         AAR11354 standard; Protein; 700 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 129pp; English.
                                                                   4;
                                     79.9%;
ilarity 79.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0512118
89US-0404679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INST BIOLOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by Epstein-Barr Virus.
                                                                                                                                                                                                                                             03-JUN-1991 (first entry)
                                                                                                                                                                                                                                                                         Cellular Receptor 2 ligand
                                                                                                                                                                                                                                                                                                                                                                                     300..312
                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAQ11140-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-101864/14.
                                      Query Match
Best Local Similarity
840 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ11140
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                                                                                                                                                                                                                                                                                                                                                                          Key
Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-1990;
08-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lernhardt W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9103251-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-1991
                                                                   31;
                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                   AAR11354;
Sequence
                                                                                                                                                               12
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vivo
                                                                                                                                                                            AAR11354
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Myers EW;

Li PWD,

Adams M,

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                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABLiG176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                            (ABBS7737-ABB72072). This patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                              Disclosure; SEQ ID NO 19548; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 2
Pred. No. 3.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 MEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.4
Best Local Similarity 43.8
Matches 14; Conservative
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14

RESULT

700 AA;

Sequence

the sequence is missing from

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Hepatitis C virus genomic RNA, DNA and related proteins - useful for detection, diagnosis and identification of hepatitis C virus
                                                                                             /note= "this part of the sequence is missing from "n. the specification"
                                                                      the specification
                                    Location/Qualiflers
1505 1520
/note= "this part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: July.29, 2002, 16:07:56 Job time: 646 sec
                                                                                                                                                                                                                                                                                                                         Claim 4; Page 16-23; 25pp; Japanese.
                                                                                                                                                                   .94JP-0223933.
                                                                                                                                                                                              , 94JP-0223933.
                                                                                                                             Ouery Match
Best Local Similarity 48.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.-4.
                                                                                                                                                                                                                         (SAYA/) SAYAMA K.
                                                                                                                                                                                                                                            WPI; 1996-182301/19.
       Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                           3023 AA;
                                                                                                                                                                                                                                                        N-PSDB; AAT13279
                                                                                                                               JP08056672-A.
                                                                                                                                                   05-MAR-1996.
                                                                                                                                                                           26-AUG-1994;
                                                                                                                                                                                                 26-AUG-1994;
                                       Peptide
                                                                                                                                                                                                                                                                                                    sub-type
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                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences (ABL01840-ABL16175) and the encoded proteins (ABB37737-ABB72072).
(ABB37737-ABB72072).
Specification, dut was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 31479; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis C virus; antibody; detection; diagnosis; vaccine; classify; subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 31479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 22;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          edgqpglwgqdlplscqscsdaascaasdlsnttc 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 QEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                      Myers EW;
                            ABB68229 standard; Protein; 2931 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR94462 standard; Protein; 3023 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                      Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.4%;
37.1%;
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11-JUL-2000; 2000US-0614150
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                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2931 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABL12332
                                                                                                                                pharmaceutical
                                                                                                                                                                            40200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                  interactions -
                                                                        26-MAR-2002
                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                      Penter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR94462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                  ABB68229
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                 ABB68229
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The present sequence is a polypeptide comprising a 3023 amino acid sequence which is encoded by a cDNA (AAT13279) to a hepatitis C virus (HCV) genomic RNA The protein can be easily detected by antibodies in an assay for the detection of HCV. The DNA and the protein are useful for classifying the subtype of HCV. At least a part of the protein may be used as a vaccine against HCV.
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                   Length 3023;
                                                                                                                                                                                                                                                                                                                                               13; Indels
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1046 glfgtivtsltgrdknvvtgevqvlstat 1074
                                                                                                                                                                                                                                                                                                                                                                                                      . 10 GLLGTLVQLLGSDDINVVTCAAGILSNLT 38
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us-09-641-104a-10.rag

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

July 29, 2002, 16:05:10 ; Search time 57.6 Seconds (without alignments) 16.538 Million cell updates/sec US-09-641-104A-10

1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

231628 seqs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 28, Appl	Sequence 100, App	Sequence 100, App		'n	ς,	30,	3,	J,	9	9	16,	Sequence 11, Appl	7, 1	7,	Sequence 2, Appli	7,	,	,	7	7	7	2,	7,	7	7	1,
SUMMARIES	ID	US-09-296-089-28	US-08-630-822A-100	US-09-005-069-100	US-08-933-227-4	US-08-219-262B-3	US-08-219-262B-5	-08	US-09-031-655-3	US-09-031-655-5	US-09-189-035-6	US-09-382-086-6	US-09-108-020-16	US-08-982-785A-11	US-08-219-262B-7	US-09-031-655-7	US-08-216-260-2	US-07-741-940-7	US-08-289-548A-7	US-08-452-654-7	US-07-741-940-2	US-08-289-548A-2	-08-452-	US-08-452-655B-2	US-08-452-655B-7	US-08-370-235A-2	US-08-450-582-2	US-08-450-582-7
	DB	4	~	~	7		7	7	e	m	m	4	4	4	1	m	N	1	Н	٦	Т	П	Н	П	1	7	m	m
	Query Match Length DB	11	178	178	529	1012	1012	1012	1012	1012	398	398	483	999	1012	1012	837	2842	2842	2842	2843	2843	2843	2843	2843	2843	84	2843
dР	Query	26.8	26.3	26.3	25.8	25.0	25.0	25.0	25.0	25.0	24.7		24.5	24.5		24.5				24.2			•	•	•	24.2	•	24.2
	Score	52	51	51	20	48.5	48.5	48.5	48.5	48.5	48	4		47.5	•	47.5	47	47	47	47	47	47	47	47	47	47	47	47
	Result No.	1	7	m	4	ιO	9	7	σο	σ	10	11	12	.13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

	Appli	Appli	Appl 1	, Appl	, Appl	Appli	Appli	Appli	Appli	Appli	, Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appli	
	,	7	7	16	16	4	4	ý	7	4	34	'n	Ť	ć	7	7	7	7	
	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	
	US-08-821-355A-7	US-09-003-687A-7	US-09-136-605-7	US-08-246-982A-16	US-08-453-265-16	US-09-740-035-4	US-09-110-517-4	US-08-843-530B-6	US-08-843-530B-2	US-08-843-530B-4	US-08-843-530B-34	US-07-551-531-2	PCT-US94-00198-1	PCT-US94-00198-2	US-08-510-284-1	US-08-411-389-2	US-08-449-933-2	US-07-966-049A-2	
	N	7	4	Н	Н	4	4	7	7	~	C)	-	ß	വ	-	Н	~	4	
	-, 2973	. 2973	. 2973	3119	3119	379	686	., 1281	1298	1298	: 1298	. 2020	. 2485	2485	2818	2818	2818	2818	
•	24:2	24.2	24.2	24.0	24.0	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	
ر :	47	47	. 47	46.5	46.5	46	. 46	46	46	. 46	46	. 46	46	46	46	. 46	. 46	46	
	28	59	30	31	32	33.	34	35: ,	36	37	38	39	40	41.	42	43	44	45	

ALIGNMENTS

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Gaps
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                                                                       APPLICANT: BLASCHIK, Orest W.
APPLICANT: Byers, Stephen
APPLICANT: Byers, Stephen
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION
FILE REFERENCE: 100086.411
CURRENT APPLICATION NUMBER: US/09/296,089
CURRENT PILLING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3:0
SEQ ID NO 28
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 11; 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Score 52;
Pred. No.
                Sequence 28, Application US/09296089 Patent. No. 6303576 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.8%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0
                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapien
US-09-296-089-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LGTLVQLLGSD 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LGTLVQLLGSD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2 US-08-630-822A-100
US-09-296-089-28
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Sequence 100, Application US/08630822A
Patent No. 5840695
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA,
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500

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COMPUTER READABLE FORM: Colorado U.S.A. STREET: 1700 ICLTY: Denver STATE: Colorac COUNTRY: U.S. 2 ZIP: 80203

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26;
                                                                                                                                                         Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Guegler; Karl
APPLICANT: Corley, Neil
APPLICANT: Shah, Purvi
AITLE OF INVENTION: HUMAN IMPORTIN ALPHA HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: OSTEMATION SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,227
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.4%; Pred. No. 26;
Matches 13; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                     8 MEGLLGTLVQLL---GSDDINVVTCAAGILSNLT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 DAVEQILPTLVRLLHHDDPEVLADTCWAISYLT 279
                                                                                                                                                                                                                                                                                                       5 VEGALGFLVEMLKYKAPSKTLAIVENAGGILRNVS 39
                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 EGMEGLLGTLVQLLGSDDINVVTCAAGILSNLT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Incyte Pharmaceuticals, Inc 3174 Porter Dr.
                                                                                                                                                                  Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
MAME: Billings, Lucy J.
REGIGSTRATION UNMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/08933227
; Patent No. 5965394
                                                                                                                                                                    26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acids
                                                                                                                                                                       Ouery Match
Best Local Similarity 40.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank CLONE: 1708480; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5965394
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA
USA
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                                                        ,
MOLECULE TYPE:
US-09-005-069-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-933-227-4
                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT ... 4,
US-08-933-227-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: HOLEN'S SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 2; Length 178; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches 10; Indels
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,82A
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTONEY/AGENT INPOMEATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 2618-17-C3
REGISTRATION NUMBER: 2618-17-C3
TELEPHONE: (303) 863-9700
TELEFAK: (303) 863-9700
TELEFAK: (303) 863-9700
TELEFAK: (303) 863-9703
TELEFAK: (303) 863-973
THYPE: AMINO ACID NO: 100: SEQUENCE CHARACTERISTICS:
LENGTH: 178 mmino acids
TYPE: amino acid
TYPE: AMINO acids
T
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 MEGLLGTLVQLL----GSDDINVVTCAAGILSNLT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-005-069-100
; Sequence 100, Application US/09005069
Patent No. 5932470
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/630,822
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CONNELL, GARY J.
RECISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 178 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.3
Best Local Similarity 40.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein
US-08-630-822A-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Colorado COUNTRY: U.S.A. ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Denver
STATE: Colora
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Gaps
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| Sequence No. S871744
| GENERAL INFORMATION:
| PAPPLICANT: VAKHARIA, Vikram N. APPLICANT: VAKHARIA, Vikram N. APPLICANT: MUNDT. Egbert
| TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
| VIWABRE OF SEQUENCES: 34
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
| STREET: 655 Fifteenth Street, N. W., STREET: Suite 330 : G Street Lobby
| STREET: DC | STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
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STATE: VIRGINIA.

ZIP: 22202
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC.COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGERENCE/DOCKET NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 27,03
TELEPRA: (703) 413-2220
TELEPRA: (703) 413-2220
TELEPRA: (703) 413-2220
TELERER: (703) 413-2220
TELEX: CARRETE OFFRET OFFRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/708,541A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query.Match 25.0%; Score 48.5; DB 1;
Best Local Similarity 37.1%; Pred. No. 98;
Matches i 13; Conservative 5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Infectious bursal disease virus STRAIN: CU-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 QTSVHGLVLGATIYLIGFDGTTVITRAVAANNGLT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 QEGMEGL-LGTLVQLLGSDDINVVTCAAGILSNLT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICS C.
REFERENCE/DOCKET NUMBER: 78,105
REFERENCE/DOCKET NUMBER: P8172-6002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .LENGTH: 1012 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-708-541A-30
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                                                                                                                              GENERAL INFORMATION:

APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDAY
APPLICANT: SNYDAY
APPLICANT: SNYDAY
APPLICANT: SNYDAY
APPLICANT: SNYDAY
APPLICANT: MENCEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: A
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08219262B
Patent No. 5788970
GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MINGEL-WHERSAY, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THERBON
TITLE OF INVENTION: THERBON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHMAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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US-08-219-262B-3
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37.1%; Pred. No. 98;
tive 5; Mismatches
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                                                    Sequence 3, Application US/08219262B
Patent No. 5788970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 37.13
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRGINIA
: USA
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US-08-219-262B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
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APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
TITLE! OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE! OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE! OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, STLVAK, MCCLELLAND, MAIER & NEUSTADT
ADDRESSEE: OBLON, STLVAK, MCCLELLAND, MAIER FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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       Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR STREET: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/031,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                       16;
Score 48.5; DB 3;
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: Infectious bursal disease virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

25.0%; Score 48.5; D

Best Local Similarity 37.1%; Pred. No. 98;

Matches 13; Conservative 5; Mismatches
                                                                                                                                      249 QTSVHGLVLGATIЎLİGFDGTTVITRAVAANNGLT 283
                                                                                                       S OEGMEGL-LGTLVOLLGSDDINVVTCAAGILSNLT 38
                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR-APPLICATION DATA:
PRIOR-APPLICATION NUMBER: US 08/219,262
PILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NUMBER: 24,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                Sequence 5, Application US/09031655
Patent No. 6017759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
'TELEFAX: (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 413-3300
TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
TYPE: amino acid
STRANDEDNESS:
     Destrical Similarity 37.1%; Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: unknown MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
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US-09-189-035-6
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US-09-031-655-5
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                                                                                                                                                                                                                                                                          18-09-031-655-5
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APPLICANT: SNVDER, DAVID B
APPLICANT: SNVDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                               Length 1012;
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                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ); ORGANISM: Infectious bursal disease virus
; STRAIN: E/DEL
US-09-031-655-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 QEGMEGL-LGTLVQLLGSDDINVVTCAAGILSNLT 38
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORREY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (703) 413-3000
TELECAX: (703) 413-3220
TELECAX: (703) 413-2220
TELECAX: (703) 413-3220
                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                  Score 48.5;
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-031-655-3
; Sequence 3, Application US/09031655
; Patent No. 6017759
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5800
TELEPAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERESTICS:
LENGTH: 1012 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOTAL TOTAL TOTAL STRANGEN ACIDS STRANGENESS:
                                                                                                                                                                                                                                                                                                                                       25.0%;
                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 37.1
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                  US-08-708-541A-30
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; Sequence 6, Application US/09189035

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TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE AND TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO CURRENT APPLICATION NUMBER: US/09/108,020A CURRENT APPLICATION NUMBER: US/09/108,020A CURRENT FILING DATE: 1998-06-30 EARLIER FILING DATE: 1997-06-30 EARLIER FILING DATE: 1997-06-01 EARLIER FILING DATE: 1997-06-01 EARLIER FILING DATE: 1998-03-02 EARLIER FILING DATE: 1998-03-02 SERLIER FILING DATE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE: OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
WUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFFWARE: FastSEQ for Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47.5; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 55;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 KQGTENLLGALSTPAVRNLAKDLGIDINVIT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPLICATION NUMBER: US/08/982,785A
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY/AGEMT'INFORMATION:
NAMME: Freeman, John W.
REGISTRATION NUMBER: 29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QEGMEGLLGTL----VQLLGSD---DINVY 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street (CIIV: Boston STREET: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence'11, Application US/08982785A Patent No. 6258929 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERA: 617/542-890b
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Arabidopsis thaliana
US-09-108-020-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.5%;
Best Local Similarity 45.2%;
Matches 14; Conservative
                 APPLICANT: Luethy, Michael H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617/542-5070 TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 666 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-982-785A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 3; Length 398;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.7%; Score 48; DB 4; Length 398, 37.1%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: COLLey, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYPOKINE SIGNAL REGULATORS
FILE REFERRNCE: PF-0638 US
CURRENT APPLICATION NUMBER: US/09/189,035
CURRENT FILING DATE: 1998-11-10
SOFTWARE: PERL FROGram
SOFTWARE: PERL FROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
CURRENT APPLICATION NUMBER: US/09/382,086
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/189,035
EARLIER FILING DATE: 1998-11-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LLGTLVQLLGSDDINV-----VTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 LLGRLTGVAGEDELQVIQPEKSVSVAAGESATLRC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LLGTLVQLLGSDDINV-----VTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 LLGRLTGVAGEDELQVIQPEKSVSVAAGESATLRC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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Patent No. 6143561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09382086 Patent No. 6201106 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.78;
37.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Randall, Douglas D.
APPLICANT: Johnston, Mark L.
APPLICANT: Miernyk, Jan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: -
CTHER INFORMATION: 92052058
US-09-382-086-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: 92052058
US-09-189-035-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 37.1 Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: SOFTWARE: PERL Program
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Best Local Similarity
Matches 13; Conserv
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US-09-108-020-16
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LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 398
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE,OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE,OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE,OF INVENTION: THEREON
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47.5; DB 3;
Pred. No. 1.4e+02;
6; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Infectious bursal disease virus 52/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET. NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
Sequence 7, Application US/09031655
Patent No. 6017759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.5%;
37.1%;
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Best Local Similarity
Matches 13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                 VIRGINIA
                                    Patent' No. 6017759
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unkr
MOLECULE TYPE: F
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-031-655-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                             Score 47.5; DB 4; Length 666; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIGILIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                          Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: OBLON, NORMAN: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELECOMMUNICATION OF TELEC
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Pred. No. 1.4e+02;
6; Mismatches 15;
                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                   7 GMEGLLG-----TLVQLLGSDDINVVTCAAGILSNLT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 QEGMEGL-LGTLVQLLGSDDINVVTCAAGILSNLT 38
                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08219262B Patent No. 5788970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.58;
37.18;
                                                                                                                                24.5%;
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Best Local Similarity 37.19
Matches 13; Conservative
                                                                                                                             Query Match 24.55
Best Local Similarity 33.33
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
            ; MOLECULE TYPE:
US-08-982-785A-11
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-219-262B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Op
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Gaps

Indels

15;

RESULT 15 US-09-031-655-7

Length 1012;

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OM protein - protein search, using sw model

July 29, 2002, 16:09:14; Search time 70.63 Seconds (without alignments) 53.058 Million cell updates/sec Run on:

US-09-641-104A-10 194 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	S35099 beta-catenin - Afr	A38973 beta-catenin - hum	beta-catenin -	T12689 armadillo segment		S33793 hypothetical prote	- plakoglobin							TŽĒJ12.6 prot		hypothetical	hypothetical	ч		aconitate hyd		T04573 hypothetical prote	phosphoglyce	F84385 dipeptide ABC tran	conserved		S75016 phosphoglycerate	
	DB	7	7	7	~	~1	~	7	~	~	7	7				~	7	7	~	7	7	~	7	-	7	7	~	7	c
	Length	781	781	781	843	806	817	738	744	820	621	678	196	964	1299	783	322	248	526	555	868	419	458	525	526	166	253	554	600
ato	Watch	100.0	100.0	100.0	79.9	77.3	75.8	67.5	0.99	61.9	58.2		33.0	33.0	32.0		28.9	28.6	28.4	28.4	28.1	27.8	٠			27.3	27.3	27.3	
	Score	194	194	194	155	150	147	131	128	120	113	7.1	64	64	9	56.5	Ω	55.5	52	S	54.5	54	54	Ŋ		23	23	n	ני
+[:::00	No.	1	7	m	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	ac

transport protein	hypothetical prote	hypothetical prote	hypothetical Armad	hypothetical prote	importin alpha (im	H+-transporting AT	subtilisilike seri	hypothetical prote	F22M8.8 protein -	Munc13-3 protein -	antimicrobial pept	hypothetical prote	probable membrane	probable membrane	band-6-protein - b
S72698	E64416	T47552	T50316	I64033	B90097	A34283	A99093	T36307	D86151	T42759	S59961	C83100	AH0265	AF0650	S60711
7	~	7	7	7	7	7	7	7	~	7	~	7	7	~	7
.1008	238	556	664	487	514	578	579	338	885	2207	80	133	214	215	295
27.1	26.8	26:8	26.8	26.5	26.5	26.5	26.5	26.3	26.3	26.3	26.0	25.8	25.8	25.8	25.8
52.5	. 52	. 52	52	51.5	51.5	.51.5	51.5	. 51	. 51	. 51	50.5	. 20	. 50	20	20
30 .	31	32	33	34	32	36	37	38	. 68	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 S35099 beta-catenin - African clawed frog C;Species: Xenopus lacvis (African clawed frog) C;Species: Xenopus lacvis (African clawed frog) C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000 C;Accession: S35099 R;McCrea, P. D; Turck, C.W.; Gumbiner, B. Science 254, 1359-1361, 1991 A;Title: A homolog of the armadillo protein in Drosophila (plakoglobin) associated w1 A;Reference number: S35099; MUD:92073903 A;Accession: S35099 A;Molecule: type: mRNA A;Residues: 1-781 <mcc></mcc>
A;Cross_references: GB:M77013; NID:g214020; PIDN:AAA496/0.1; PID:g214021 C;Keywords: cytoskeleton C;Keywords: cytoskeleton Query Match Best Local Similarity 100.0%; Pred. No. 8.2e-18; Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy .1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 RESULT 2 A38973 beta-catenin - human C;Species: Homo sapiens (man) C;Date: 26~Jan-1996 #sequence_revision 08-Feb-1996 #text_change 08-Oct-1999 C;Accession: A38973; S55356; S31988
 R:Huelsken, J.; Birchmeier, W.; Behrens, J. J. Cell Biol. 127, 2061-2069, 1994 A;Title: Biol. 127, 2062 compete for the interaction with beta-catenin and the cyt. A;Reference number: A38973; MUID:95105247 A;Scatus: A28973 A;Status: A28973 A;Status: A28973 A;Status: A28973 A;Status: A28973
A; Residues: 1-781 <hue> A; Residues: 1-781 <hue> A; Cross references: GB:219054; NID:938519; PIDN:CAA79497.1; PID:938520 A; Experimental source: placenta R; Nollet, F:: Berx, G:; Molemans, F:; van Roy, F. submitted to the EMBL Data Library, June 1995 A; Description: H: sapiens beta-catenin mRNA. A; Reference number: \$55356 A; Accession: \$55356 A; Accession: \$55356 A; Accession: Scothannary</hue></hue>
 A; Molecule type: mRNA A; Residues: 1-781 <nol> A; Cross-references: EMBL:X87838; NID:g1154853; PIDN:CAA61107.1; PID:g860988 C; Comment: The cytoplasmic protein beta-catenin normally binds to a region in the cyt</nol>

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Gaps

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Indels

Length 843;

Score 155; DB 2; Pred. No. 1.4e-12;

4; Mismatches

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C) Accession: J4835.
C) Accession: J4835.
R; Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T. Cene 172, 155-159, 1996.
A; Fitle: Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadill A; Reference number: J4835; MUID: 96257271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic.acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-806 <HOB>
A;Cross-references: GB:U36781; NID:g1407600; PIDN:AAC47137.1; PID:g1407601
C;Comment: This protein plays roles in cadherin-mediated cell adhesion and in signal
                                                                                                                                                                                                                                                                                                                                                                 C;Species: Hydra magnipapillata
C;Date::15:Aug-1996; #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                     451 ATKQDGLEGLLQMLVQLLSSNDINVVTCVSGIISNLTC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                              AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
      A)Cross_references; relybase: FBgn0000117
A;Introns: 11/1; 557/3; 624/3; 715/3; 748/1
                                                                                                                                                                                                                                                                                                                                          beta-catenin - Hydra magnipapillata
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                                                                                                                         similarity 79.5%;
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Best Local Similarity 76.3
Matches 29; Conservative
                                                                                                                                                                    Conservative
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Best Local Similarity
Matches , 30; Conserv
                                                                   C; Keywords: cytoskeleton
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A; Residues: 1-817 <ROS>
                                                                                                                       Query Match
Best. Local Simi
Matches: 31;
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                                                A; Note: 086E4.6
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A:Gene: arm
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                  poly
    microfilament network.
C;Comment: Cellular levels of beta-catenin are regulated in part by the adenomatous I cancerous cell growth.
G cancerous cell growth.
G;Genetics:
A;Gene: GDB:CTNNB1; CTNNB
A;Cross-references: GDB:41922; OMIM:116806
A;Cross-references: 3P22-3P21.3
A;Map position: 3P22-3P21.3
C;Keywords: apoptosis; carcinogenesis; cell adhesion; cytosol
F;151-676/Region: 40-residue repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Specials: Mus musculus (house mouse)
C; Specials: Mus musculus (house mouse)
C; Specials: Mus musculus (house mouse)
C; Scacesion: 355091
R; Butz, S.; Stappert, J.; Weissig, H.; Kemler, R.
Science 257, 1142-1144, 1992
A; Title: Plakoglobin and beta-catenin: distinct but closely related.
A; Reference number: 355091; MUID: 92376536
A; Accession: S35091
A; Scatus: preliminary
A; Molecule type: mRNA
A; Residues: 1-781 < Butz, A; Molecule type: mRNA
A; Residues: 1-781 < Butz, A; Molecule type: mRNA
A; Residues: 1-781 < Butz, Molecule type: mRNA
A; Residues: cytoskeleton
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                                                                                                                                                                                                                                                         Gaps
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A;Residues: 1-843 <RIG>
Cross-references: EMBL:X54468; NID:97610; PIDN:CAA38350.1; PID:97611
C;Genetics:
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                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 194; DB 2;
; Pred. No. 8.2e-18;
0; Mismatches 0;
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                                                                                                                                                                                                                 100.0%; Score 194; DB 2;
llarity 100.0%; Pred. No. 8.2e-18;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                    1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                            1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
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ilarity 100.0%;
Conservative 0
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Best Local Similarity
Matches 39; Conserv
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Best Local Similarity
Matches 39; Conserv
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Gaps

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Score 150; DB 2; Length 806; Pred. No. 6.3e-12; 5; Mismatches 4; Indels

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hypothetical protein - spoonworm (Urechis caupo)
hypothetical protein - spoonworm (Urechis caupo
C.Species: Urechis caupo
C.Date: 19; Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C.Accession: S33793
B.Cochim: Biophys. Acta'1173, 337-341, 1993
A.Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two
A.Reference number: S33793; MUID: 93305730
A.Reference number: S33793; MUID: 93305730
A.Scession: S33793;
A.Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                     75.8%; Score 147; DB 2; I .76.9%; Pred. No. 1.6e-11; ative 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plakoglobin - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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A:Status: preliminary A:Molecule, type: mRNA A:Residues: 1-820 <ROS>

A; Accession: S33794

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A) Experimental source: clone K05C4
R;Costa, M; Raich, W; Agbunag, C.; Hardin, J.; Priess, J.R.
submitted to the EMBL Data Library, July 1997
A;Description: A putative catenin-cadherin system mediates morphogenesis of the C. el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHarris, B.
submitted to the EMBL Data Library, November 1996
Submitted to the EMBL Data Library, November 1996
A: Reference number: 219729
A: Reference number: 21341
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-678
A: Cross-references: EMBL: 281564; PIDN: CAB04572.1; GSPDB: GN00019; CESP: K05C4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date:~06.Jan-1995 #sequence_revision 06.Jan-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                 Gaps
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R; Butz, S; Stappert, J; Weissig, H.; Kemler, R.
Science: 257, 1142-1144, 1992
A; Title: Plakoglobin and beta-catenin: distinct but closely related.
A; Reference number: S35091; WUID: 92376536
A; Accession: S35092
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                                                                                                                                                           Score 120; DB 2;
Pred. No. 6.5e-08;
3; Mismatches 6
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Pred. No. 4.2e-07;
4; Mismatches 10
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                                                                                                                                                                                                                                                                                         6 EGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
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A; Introns: 14/1; 235/1; 290/1; 620/3
                                                                                                                                                           Ouery Match
Best Local Similarity 73.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.2%;
Best Local Similarity 62.2%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Residues: 1.621 <BUT>
A, Cross-references: EMBL:M90365
C, Keywords; cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                - mouse (fragment)
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 29-Aug-1997
C;Accession: A32905
R;Franke, W.W.; Goldschmidt, M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cowin, Proc. Natl. Acad. Sci. U.S.A. 86, 4027-4031, 1989
A;Title: Molecular cloning and amino acid sequence of human plakoglobin, the common jund A;Reference number: A32905; MUID:89264555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Tripneustes gratilla
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C.Accession: 533794
R.Rosenthal, E.
Biochim. Biochys. Acta 1173, 337-341, 1993
A.Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver
A.Reference number: 533793; MUID:93305730
C;Species: Xenopus laevis (African clawed frog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S35093; S24636
R;Fouquet, B.; Zimbelmann, R.; Franke, W.W.
Differentiation 51, 187-194, 1992
A;Title: Identification of plakoglobin in oocytes and early embryos of Xenopus laevis: A;Reference number: S35093; WUID:9309332
A;Accession: S35093
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R;Demarais, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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hypothetical protein - sea urchin (Tripneustes gratilla)
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNÅ
A;Residues: 133-144,'V',186-225,'T',227-292 <DEM>
A;Cross-references: EMBL:X67078; NID:965252; PID:965253
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 131; DB 2;
Pred. No. 2e-09;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 128; DB 2,
Pred. No. 5e-09;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1992 A; Reference number: $24636 A; Accession: $24636 A; Accession: $24636 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:126565; OMIM:173325
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65.8%;
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65.8%;
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Best Local Similarity 65.8
Matches 25; Conservative
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C;Genetics:
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C; Keywords: cytoskeleton
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-738 <FOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-744 <FRA>
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Chin, C.W.; CKERT, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
A, Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo kar, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zam protein [imported] - Anabaena sp. (strain PCC 7120)
C.Species: Anabaena sp.
A.Note: Anabaena sp.
A.Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
A.Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C.Accession: AE1961
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Rakasaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata NRA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Recession: AE1961
A.Accession: AE1961
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: zam
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE005172; NID: 92829894; PIDN: AAC00602.1; GSPDB: GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62;
Pred. No.
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Job time: 726 sec
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739 ILRLLISFLEDDDVNVKEAAGGVLANL 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LLGTLVQLLGSDDINVVTCAAGILSNL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.0%;
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Best Local Similarity 43.3
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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A; Molecule type: DNA
A; Residues: 1-1299 <STO>
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                            hypothetical protein wrm-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03746
R;Rochelaud, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; Prie
Cell 90, 707-716, 1997
A;Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embra
A;Reference number: 215051; MUID:97433081
A;Recession: T03746
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-796 - RNCO
A;Residues: 1-796 - RNCO
A;Residues: 1-796 - RNCO
A;Residues: 1-796 - RNCO
A;Residues: 1-796 - RNEL:AF013951; NID:92343264; PIDN:AAC47748.1; PID:92343265
A;Conserimental source: strain Bristol
C;Genetics:
A;Genetics:
A;Map position: 3
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G;Genetics:
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C;Species: Caenorhabditis elegans
C;Datte: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15342
R;Taich, A.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
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A;Introns: 132/3; 152/1; 188/1; 245/3; 373/3; 667/1; 782/3; 838/2; 906/1
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A; Description: The sequence of C. elegans cosmid B0336
                                                                            15;
                                                                                                                                                                                 321 SATNEENLTOLIIKLLEIIRVANDGMTACACGTLSNLTC 359
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                                                                                                                                1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
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33.0%; Score 64; DB 2
Best Local Similarity 33.3%; Pred. No. 2.3;
Matches 12; Conservative 10; Mismatches
                                                 Local Similarity 35.9%; Pred. No. 0.19 nes 14; Conservative 10; Mismatches
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A; Accession: T15342
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Best Local Similarity
Matches 12; Conserv
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प्रकार केरा प्राप्त के इस्त है। इस्त प्राप्त का अपने प्राप्त करते हैं। इस्त प्राप्त के प्राप्त के प्राप्त के अ जिसम्माद्य महिन्द्रमान महिन्द्रमान के बहुन है। असे का सम्पर्त के स्वर्ण के अस्त है। इस महिन्द्र के अपने स्वर्ण

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 16:09:54; Search time 34.24 Seconds (without alignments) 44.102 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-641-104A-10 194 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P35222 homo sapien	mus m			_	_	Q02453 musca domes	P30998 xenopus lae	Q02257 mus musculu	P14923 homo sapien	•					_	Q58343 methanococc		_	P80398 rana rugosa		mus m	Q28161 bos taurus	P97350 mus musculu	Q13835 homo sapien	haemo	Q57991 methanococc		_	_			P16256 escherichia
SUMMARIES	ID	CTNB_HUMAN	CTNB_MOUSE	CTNB_RAT	CTNB_XENLA	ARM_DROME	CTNB_URECA	ARM_MUSDO	PLAK_XENLA	PLAK_MOUSE	PLAK_HUMAN	CTNB_TRIGR	Y787_SYNY3	ACO2_SYNY3	SERA_BACSU	SERA_SYNY3	MMLA_MYCLE	Y933_METJA	VPL_HAEIN	VATA_METBA	GAE4_RANRU	IMA2_HUMAN	IMA2_MOUSE	PKP1_BOVIN	PKP1_MOUSE	PKP1_HUMAN	YAJF_HAEIN	AK_METJA	END4_THENE	Y267_BUCAI	END4_THEMA	DHYS_AERPE	HTPX_STRGC	PANF_ECOLI
	DB	1					П											П	П	П	Т	1	-	1	٦	٦	-			-	-	Н	-	П
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ď	Ouery Match	100.0	100.0	100.0	100.0	79.9	75.8	74.2	67.5	0.99	0.99	61.9	28.9	28.1	27.8	27.3	27.1	26.8	26.5	26.5	26.0	25.8	25.8	25.8	25.8	25.8	25.5	25.5	25.3	25.3	25.3	25.3	25.3	25.3
	Score	-	194	194	σ	155	147	144	131	128	128	120	26	54.5	54	S	52.5	S	٠	51.5		20	20	20	20		5					49	49	49
	Result No.	н	Ö	æ	4	S	9	7	ω.	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

	Q19969 caenorhabdi	P52296 rattus norv	-	P70168 mus musculu	P15480 avian infec	P94368 bacillus su	032434 propionibac	Q04173 bos taurus	P52306 homo sapien	Q9si64 arabidopsis		Q92g96 rickettsia			
	IMA_CAEEL	IMB1_RAT	IMB1_HUMAN	IMB1_MOUSE	POLS_IBDVC	YXKO_BACSU	PPOX_PROFR	GDS1_BOVIN	GDS1_HUMAN	SPE1_ARATH	NUOM_RICPR	NUOM_RICCN		ALIGNMENTS	
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•	25.3 514	25.3 875	25.3 876	25.3 876	25.0 .1012	24.7 276	24.7 . 527	24:7 . 558	24.7 558	24.7 702	24.5 :: 491	24.5 493	5		
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ALIGNMENTS

RESULT 1 CTNB_HUMAN 1 CCC CC
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MEDLINE-20337986;
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361
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142
189
                                alpha-catenin.
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Q9WU82;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 118-149 IN COMPLEX WITH
                                                                         Interpro; IPR001255, Armadillo...
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
PR051TE; PS50176; ARM; EPERAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92376536; PubMed=1509266; MEDLINE-92376536; PubMeds S., Stappert J., Weissig H., Kemler R.; Plakoglobin and beta-catenin: distinct but closely related."; Science 257:1142-1144(1992).
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                                                                                                                                                                                                                                                   Length 781;
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"Regulation of beta-catenin signaling in the Wnt pathway.";
Biochem. Biophys. Res. Commun. 268:243-248(2000).
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                                                                                                                                                                                                                           CB78F165A3EEF86E CRC64;
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                                                                                                                                                                                                                                                  100.0%; Score 194; DB 1;
100.0%; Pred. No. 5.7e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
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Last annotation update)
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MEDLINE=97442350; PubMed=9298899;
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                           EMBL; X87838; CAA61107.1; -.
                                   EMBL; Z19054; CAA79497.1;
PIR; S31988; S31988.
PDB; 1G3J; 17-JAN-01.
TRANSFAC; T02872; -.
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
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3318
3389
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484
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                                                                                                                     Repeat; 3D-structure
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                            181 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Beta-catenin
                                                                     MIM; 116806;
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CTNB_MOUSE
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                                                                                                                                                                        THE CYTOSTICATION THE REGULATION OF CELL ADHESION AND IN CYTOSTICATION THROUGH THE WNT PATHWAY.

SIGNAL TRANSDUCTION THROUGH THE WNT PATHWAY.

SIGNAL TRANSDUCTION THROUGH THE WNT PATHWAY.

SIGNAL TRANSDUCTION THROUGH THE WNT PATHWAY.

CHARLES DEGRAPATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APPC AND CYTOSTICATION. THE CYTOSOLIC FORM BINDS TCF/LEF-1 AND MAY ALSO BIND CYTOSTICATION. THE NUCLEAR FORW BINDS TCF/LEF-1 AND MAY ALSO BIND COPTINES. THE ANCHORAGE CYTOSTICATION THE COPPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE CYTOSTICATION. CYTOSTELLIZED (HIGH CYTOSTELLIZED (HIGH CYTOSTELLIZED CHOW EXPEL OF PHOSPHORYLATION). TRANSLOCATION.

CHARLELIZED (LOW EFFEL OF PHOSPHORYLATION).

CHARLETZED (LOW EFFEL OF PHOSPHORYLATION).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                Pokutta S., Weis W.I.; "Structure of the dimerization and beta-catenin-binding region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULTING IN ITS ACCUMULATION IN CYTOPLASM.
SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
SIMILARITY: CONTAINS 12 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 194; DB 1;
100.0%; Pred. No. 5.7e-18;
5+ive 0; Mismatches 0;
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PubMed=10882138;
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InterPro; IPR000225; Armadillo.
Pfem; PF00514; Armadillo_seg; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85470 MW;
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                                                                                                                                                        Cell 5:533-543(2000)
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PDB; 3BCT; 19-NOV-97.
PDB; 1DOW; 12-JUL-00.
TRANSFAC; T02984;
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1 AATKOEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC

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                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)

SIMILARITY)

-1- SUBCELLULAR LOCATION: CYTOPLASMIC WHEN IT IS UNSTABILIZED (HIGH
LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS
STABILIZED (LOW LEVEL OF PHOSPHORYLATION) (BY SIMILARITY).

-1- TISSUE SPECIFICITY: EXPRESSED IN THE TESTIS.

-1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED AT E30-60 DAY DPC IN THE
TESTIS. REDUCED EXPRESSION AT E90 DAY DPC.

-1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B. WNT-DEPENDENT ACTIVATION
OF DVL ANTAGONIZES THE ACTION OF GSK-3B. PHOSPHORYLATION OF BETA-
CATENIN IS REDUCED AND THE PROTEIN IS NO LONGER DEGRADED,
RESULTING IN ITS ACCUMULATION IN CYTOPLASM (BY SIMILARITY).

-1- SIMILARITY: ODNTAINS 12 ARM REPEATS.
                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN SIGNAL TRANSDUCTION THROUGH THE WAT PATHAXY (BY SIMILARITY).
SIGNAL TRANSDUCTION THROUGH THE WIT ALLOWS THE STIMULATION OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERRACTS WITH APC AND E-CADHERIN. THE NUCLEAR FORM BINDS TCF/LEF-1 AND MAY ALSO BIND PONTINS AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX TO THE CORTICAL ACTION (BY
                                                                                                                                                                           STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis; MEDLINE=99428593; PubMed=10497305; Chung S.S.W., Lee W.M., Cheng C.Y.; "Study on the formation of specialized inter-Sertoli cell junctions in vitro.":
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9C29186B6DD54B87 CRC64;
                    Last sequence update)
Last annotation update)
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ARM 8.
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ARM 12
                                                                                                                                                                                                                                                       J. Cell. Physiol. 181:258-272(1999)
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Pfam; PF00514; Armadillo_seg; 12.
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TrterPro; IPR000225; Armadillo.
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      Created)
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                                                                                 Rattus norvegicus (Rat).
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16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 01-MAR-2002 (Rel. 41,
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594
637
781 AA;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=10116;
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1193
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                                                   Beta-catenin.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                     WHICH
                                                                                                                                                                                                                                                                                                                                                                SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION PROPERTIES: ESSENTIAL COMPONENT OF THE VERTEBRATE WNT-SIGNALING PATHWAY AND IS REQUIRED FOR FORMATION OF THE EMBRYONIC AXIS.

SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                    -1. FUNCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE) PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WH
                                                                                                                                                                                                                                          McCrea P.D., Turck C.W., Gumbiner B.M.; "A homolog of the armadillo protein in Drosophila (plakoglobin) associated with B-cadherin."; Science 254:1359-1361(1991)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3ECD27232239F799 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 194; DB 1;
Pred. No. 5.7e-18;
; Mismatches 0;
                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
               781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bestriccal Similarity 100.0%; Pred. No. 5.7
Matches 39; Conservative 0; Mismatches
                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                       Xenopus laevis; (African clawed frog)
                 PRT;
                                                                                                                                                                                                              TISSUE-Brain;
MEDLINE-92073903; PubMed=1962194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
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InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M77013; AAA49670.1; -.
         STANDARD;
                                                                                                                                                   Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIŘ; S35099; S35099.
HSSP; Q02248; 2BCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 AA;
                                                                                                                                                                   NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell ádhesion
                                                                                           Beta-catenin
                 CTNB_XENLA
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REPEAT
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CTNB_XENLA
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141 AATKOEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC

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Gaps

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0

Mismatches

. 0

Conservative

Best_Local Similarity Matches 39; Conserv

Query Match

Length 781; Indels

100.0%; Score 194; DB 1; 100.0%; Pred. No. 5.7e-18;

us-09-641-104a-10.rsp

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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Ray Sutton G.G., Wortunan J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Basu A., Baxendle J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broxelier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Canter A.,
Berson K.Y., Dupp L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Rerisca M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Rerisca S., Rielschmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Rerisca S., Rielschmann R.J.,
Randolek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harvey D., Heiman T.J., Hennandez J.R., Houck J.,
Harvey D., Heiman T.J., Hennandez J.R., Houck J.,
Harvey D., Heiman T.J., Weil M.-H., Ibseywa C.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Multhin M., Mulby B., Murby L., Muzry D.M., Nelson R.,
Randont S.M., Moy M., Murby B., Murby L., Muzry D.M., Nelson R.,
Randont S.M., Moy M., Murby B., Murby L., Wang X.,
Randont S.M., Moy M., Wolley R., Supuski M.P., San E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Wang Z.-Y., Wangsarman D.A., Wolley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Wooge T., Worley K.C., Wu D., Yang S., Zao Q., Zhang G., Zhao Q., Zhang G., Zhang G., Zha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riggleman B., Wieschaus E., Schedl P.; "Molecular analysis of the armadillo locus: uniformly distributed transcripts and a protein with novel internal repeats are associated with a Drosophila segment polarity gene."; Genes Dev. 3:96-113(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loureiro J., Peifer M.; "Roles of Ammaillo, a Drosophila catenin, during central nervous system development."

Curr. Biol. 8:622-632(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND ALTERNATIVE
                                                                                                                                                                                                                      P18824, 002371; 09W346; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 01-NOV-1900 (Rel. 16, Last sequence update) Armadillo segment polarity protein. ARM or EG: 86E4.6 0R CG1579. Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
391 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89211895; PubMed-2707602;
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                                                                                                                                                                                              STANDARD;
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 Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND FROM
                                                                                                                                     Beros P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barreil B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadeu E.,
Dreano S., Gloix S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafáros F.C., Louis C., Siden Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkloti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Pelfer M., Pai L.-M., Casey M.; "Phosphorylation of the Drosophila adherens junction protein Armadallo: roles for wingless signal and zeste-white 3 kinase."; Armadallo: roles for wingless signal and zeste-white 3 kinase."; Dev. Biol. 166:543-556(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBRYONIC TISSUE TO TISSUE. SGG IS REQUIRED FOR PHOSPHORYLATION AND WG SIGNAL NEGATIVELY REGULATES ARM PHOSPHORYLATION.
HYPOPHOSPHORYLATED FORM OF ARM INCREASES IN STEADY-STATE LEVELS.
SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
SIMILARITY: CONTAINS 12.5 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERSEGEMNTAL NEAVES.

1. ACCOMULATE IN THE PNS.

1. DECUDIDATE IN THE STATE TO MID-EMBRYOGENESIS.

1. PHOSPHORYLATED ON SER, THR AND TYR RESIDUES. LEVEL OF PHM: PHOSPHORYLATED ON SER, THR AND TYR RESIDUES. LEVEL OF PHOSPHORYLATION VARIES BOTH DURING EMBRYONIC DEVELOPMENT AN PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                             "From sequence to chromosome: the tip of the X chromosome of D.
   s:
Zhong F.N., Zhong W., Zhou X., Zhu S., Myers E.W., Rubin G.M., Venter J.C.; sequence of Drosophila melanogaster.";
                                                                                    SEGUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMEL; AF001213; AAB59731.1; -. EMBL; AE001213; AAB59731.1; -. EMBL; AE001106; CAA15946.1; -. EMBL; AL021086; CAA15946.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, ALOZ1086; CAA15946.1; JOINED. EMBL, ALOZ1086; CAA15935.1; -. EMBL, ALOZ1106; CAA15935.1; JOINED. PIR; A31861; A31861.
                                                                                                                     MEDLINE-20196011; PubMed-10731137;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95113174; PubMed=7529201;
                                                    Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                 Science 287:2220-2222(2000).
                                                                                                            STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                     melanogaster.
                                                                                                                                                                                                                                                                                                  Glover D.M.;
   Zheng X.H.,
Gibbs R.A.,
                                         genome
                                         "The
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                     Armadillo segment polarity protein
                                                            InterPro: IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
Amari; Sm00185; ARM; III.
PROSITE; PS50176; ARM REPEAT; 9.
Cell; adhesion; Cytoskeleton; Stru
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Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
                                                                                                                                                                                             89070 MW;
                                        EMBL; L10355; AAA30330.1; -. HSSP; Q02248; 2BCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L04874; AAA29292.1; -.
                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.9
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                        451
495
541
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                                                                                                                                                           501
543
648
818 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCFI_TaxID=7370;
                                                                                                                                                                                                                                                                                                                                                ARM_MUSDO
                                                                                                                                                                                             SECUENCE
                                                                                                                                       REPEAT
REPEAT
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                                                                                                                                                                                                                                                                               LGPEEAYEGLYGQGPPSVHSSHGGRAFHQQGYDTLPIDSMQ
                                                                                                                                                                                                                                                                                        GLEISSPVGGGGÄGGAPGNGGAVGGASGGGGNIGAIPPSGA
PTSPYSMDMDVGEIDAGALNFDLDAMPTPPNDNNNLAAWYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in two invertebrates, Urechis caupo and Tripmeustes gratilia.";
Biochim. Biophys. Acta 1173:337-341(1993).
-!- FUNCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL
ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of homologues to beta-catenin/plakoglobin/armadillo
              TRANSFAC; T02977; --
FlyBase; FB900000117; arm.
InterPro: IPR000225; Armadillo.
Ffam; PF0014; Armadillo.seg; 12.
SWART; SW00185; ARW; 11.
SWART; SW00185; ARW, REPEAT; 9.
Developmental protein; Segmentation polarity protein; Repeat; Cell adhesion; Cytoskeleton; Structural protein; Phosphorylation; Alternative Splicing.
                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urechis caupo (Innkeeper worm) (Spoonworm).
Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
NCBI_TaxID=6431;
                                                                                                                                                                                                                                                                                                               TDC -> ILYQ (IN NEURAL ISOFORM)
40DAD6FB83163049 CRC64;
                                                                                                                                                                                                                                                                                                                                                        Score 155; DB 1; Length 843;
Pred. No. 8.5e-13;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPERTIES.
SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
SIMILARITY: CONTAINS 7 ARM REPEATS.
                                                                                                                   ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                     ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                           (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                                                               1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 28, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-93305730; PubMed-8318544;
                                                                                                                                      ARM
ARM
ARM
ARM
ARM
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ARM
ARM
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                                                                                                                                                                                                                                                                                                                          91152 MW;
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79.58;
                                                                                                                                                                                                                                                                                                                                                                              31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 28, (Rel. 28,
                                                                                                                                                                                                                                                                                                                         843 AA;
         HSSP; 002248; 1DOW.
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 31; Conserv
                                                                                                                                       201
243
3243
341
4411
4411
4497
5539
6699
648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal E.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTNB_URECA P35224;
                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                               REPEAT
REPEAT
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REPEAT
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REPEAT
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or'send an email to license@isb-cib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Musca domestica (House fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Musca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 818;
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-1: SUBCELLULAR LOCATION: INNER SURFACE OF CELL MEMBRANE.

-1: SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.

-1: SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                     ARM 1.
ARM 2.
ARM 3.
ARM 3.
ARM 5.
ARM 6.
ARM 6.
ARM 7.
ARM 7.
                                                                                                                                                                   Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 AATKSSDIEGLLQMLVQLLASNDINIVTCAAGILSNLTC 451
                                                                                                                                                                                                                                                                                                                                                                                                     75.8%; Score 147; DB 1; 76.9%; Pred. No. 9.3e-12; iive 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              813 AA.
orfsend an email to.license@isb-sib.ch)
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PRT;
                                                      PIR: 524636; S24636.
PIR: 535093; S35093.
HSSP: 002248; 25267;
HTC-Pro: IPR000225; Armadillo.
Pfam: iPP00514; Armadillo.seg; 11.
SWART; SM00185; ARM; 10.
                                                                                                                                                                   ARM
                                                                                                                                                                              ARM
                                                                                                                              PROSITE; PS50176; ARM_REPEAT; 9.
                                                                                                                                                                                                                                                                                              81711 MW;
                                                                                                                                                                                                                                                                                                                               67.5%;
                                                                                                                                         Cytoskeleton;
                                  EMBL; M95593; AAA49931.1;
EMBL; X67078; CAA47463.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2] REVISIONS TO 294 AND 296.
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (Mouse).
                                                                                                                                                                                                                                                                                            738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATED FORM
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                             419
466
508
570
                                                                                                                                            adhesion;
                                                                                                                                                                                                                                                                                                                                                   Matches' 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLAK_MOUSE
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                       REPEAT
                                                                                                                                                                   REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEV. Biol. 153:337-346(1992).

-1- FUNCTION: COMMON JUNCTIONAL PLAQUE PROFEIN. THE MEMBRANE-ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE PRESENCE OF BLAKOGLOBIN IN 1N BOTH THE DESMOSOMES AND IN THE INTERNEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDIINE-9309332; PubMed=1459359;
Fouquet B., Zimbelmann R., Franke W.W.;
"Identification of plakeglobin in occytes and early embryos of Xenopus laevis: maternal expression of a gene encoding a junctional
                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
1-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III).
Sknopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                          ;
0
             polarity protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Marais A.A., Moon R.T.;
"The armadillo homologs beta-catenin and plakoglobin are
differentially expressed during early development of Xenopus
                                                                                                                                                                                                    Length 813;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                73E61F59BDBFA580 CRC64;
                               ASP/GLU-RICH (ACIDIC).
ARM 1.
ARM 3.
ARM 4.
ARM 6.
ARM 6.
ARM 7.
ARM 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 10 ARM REPEATS.
                                                                                                                                                                                                  Score 144; DB 1; I
Pred. No. 2.3e-11;
; Mismatches 5;
                                                                                                                                                                                                                                                             389 AATKVDGLEPLLQSLVQVLASTDVNVVTCAAGILSNLTC 427
                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
                                                                                                                                                                                                                                                                                                                               738 AA
                                                                                                                                                                                                                        5; Mismatches
                        Structural
        orotein; Segmentation
Cytoskeleton; Structu
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 133-292 FROM N.A. MEDLINE=93012479; PubMed=1397690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Differentiation 51:187-194(1992).
PS50176; ARM_REPEAT; 9
                                                                                                                                                                88237 MW;
                                                                                                                                                                                                 74.2%;
ilarity 74.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                STANDARD;
            Developmental protein;
Sell adhesion; Cytoskel
                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATED FORM
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                813 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plaque protein.";
                                                                                          349
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                               PLAK_XENLA
 PROSITE;
                                                                                                                                                                SEQUENCE
                                                        REPEAT
REPEAT
REPEAT
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                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laevis
                                               REPEAT
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                                   DOMAIN
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entities requires'a license agreement (See http://www.isb-sib.ch/announce/
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1-- SUBUNIT: HOMODIMER.
-1-: SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.7. MEDLINE=92376536; PubMed=1509266; MEDLINE=92376536; PubMed=1509266; Memler R.; Butz, S., Stappert J., Weissig H., Kemler R.; Plakoglobin and beata-catenin: distinct but closely related."; Science 257:1142-1144(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                  Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I -> V (IN REF. 2).
A -> T (IN REF. 2).
569DBE69D08BBC58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01.JUL-1993 (Rel. 26, Created)
1.JUL-1993 (Rel. 34, Last sequence update)
01.MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 131; DB 1;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ATKOEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                     or send an email to license lisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                 ARM 5.
ARM 5.
ARM 6.
ARM 7.
ARM 9.
ARM 9.
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0
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MEDLINE-8926455; PubMed-2726765;
Franke W.W., Goldschnidt M.D., Zimbelmann R., Mueller H.M.,
Schiller D.L., Cowin P.;
"Molecular cloning and amino acid sequence of human plakoglobin, the
common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:40274031(1989).

-:- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE PRESENCE OF PARKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-ASSOCIATED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                            Cell adhesion; Cytoskeleton; Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                             17CF444607422BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY SIMILARITY: CONTAINS 8 ARM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 128; DB 1;
Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 ATKQEGLESVLKILVNQLSVDDVNVLTCATGTLSNLTC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                    PIR; S35092; S35092.
HSSP; Q02246; DDW.
MGD; WG1:96650; Jup.
InterPro; IPR000225; Armadillo.
Pfan; PR00144; Armadillo_seq; 11.
SMART; SM00185; ARM; 8.
PROSITE; PS50176; ARM.REPEAT; 9.
                                                                                                                                                                                                                                                                         ARM
ARM
ARM
ARM
ARM
ARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                             68111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0%;
65.8%;
                                                                                                                       EMBL; M90365; AAB02885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                      131
173
257
296
                                                                                                                                                                                                                                                                                                                                                                                                            621 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                       92
1134
2259
2299
3388
450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAK_HUMAN
P14923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of homologues to beta-catenin/plakoglobin/armadillo in two invertebrates, Urechis caupo and Tripneustes gratilla."; Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Brobys. Acta 1173:337-341(1993).

-i- FUNCTION. BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE) PROTEINS. THE ASSOCIATION OF CAPENINS TO CADHERINS PRODUCES ASSEMENT OF ILL SIGNED TO THE ACTIN FILAMENT NETWORK, AND WHICH SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tripneustes gratilla (Hawaian sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                            ARM 2.
ARM 4.
ARM 4.
ARM 5.
ARM 5.
ARM 6.
ARM 7.
ARM 7.
ARM 8.
GQLA -> DSSL (IN REF. 1; AAA64895).
V -> A (IN REF. 1; AAA64895).
W; 472741F400D388FD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                 Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The properties:

The similarity: Belongs to the beta-catenin family.

Similarity: Contains 10 arm repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 128; DB 1; L
Pred. No. 2.7e-09;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ATKQEGMEGILGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last Sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   820 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                  PROBABLE
                                                                                                                                                                                                                                                                                                  ARM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                HSSP, 002248; ZBCT.
MIM: 173325; -
Interpro: IPR000225; Armadillo.
Ffam: PF00514; Armadillo_seg; 10.
SMART; SM0185; ARM: 8.
PROSITE: PS50176; ARM REPEAT; 8.
Cell adhesion; Cytoskeleton; Struct
INIT_MET 111 179 ARM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=93305730; PubMed=8318544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              81498 MW;
                                                                                                                                  EMEL; M23410; AAA64895.1; -. PIR; A32905; A32905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.0%;
65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.0
Best Local Similarity 65.8
Matches 25. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            478
582
96
139
743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tripneustes.
NCBL_TaxID=7673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenthal E.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTNB_TRIGR
                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
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CTNB_TRIGR
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This
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Length 322;

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us-09-641-104a-10.rsp

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EGMEGLLGT:-----LVQLLGSDDINVVTCAAGILS 35
OuerykMitch
Best Local Similarity 31:68;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 15, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761
                                                                                                                                                                                                                 ACNB OR SLR0665.
                                                                                                                                                                                                                                                 NCBI TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOCITRATE
                                                                                                                                                                                                         Aconitase 2
                                                                                                                                   ACO2 SYNY3
P74582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                            13
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                                                                                                                        ACO2_SYNY3:
                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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        and for commercial
                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-96127529; PubMed-8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                      Length 820;
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                         Structural protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l protein; Complete proteome.
322 AA; 34723 MW; C8B434C5B3C0460D CRC64;
         ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                      57255E0F57795FD3 CRC64;
           Usage
                                                                                                                                                                                                                                                                                                                            .
.
                                                                                                                                                                                                                                                                                                     Score 120; DB 1;
Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 322 AA
           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                     EGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence ul
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical 34.7 kDa protein sll0787
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D64005; BAA10714.1; -...
InterPro; IPR000728; AIRS_related.
Fem; PF00586; AIRS; I.
Pfam; PF02769; AIRS_C; I.
                                                                                                                                                    ARM
ARM
ARM
ARM
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ARM
                                                                      PIR; S33794; S33794.

HSSP; Q02248; IDOW.

InterPro; IPR000225; Armadillo.

FF00514; Armadillo_seg; 12.

SMART; SM0185; ARM; 12.

PROSITE; PS50176; ARM_REPEAT; 9.
                                                                                                                                                                                                                                                                        Ψ.
                                                                                                                                                                                                                                                                                                       61.9%;
ilarity 73.5%;
Conservative
                                                                                                                                           Cytoskeleton;
                                                        EMBL; L10354; AAA30089.1; -.
                                                                                                                                                                                                                                                           683
89361
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                                                                                                                                                                                       322
4405
4489
535
642
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                       820 AA;
                                                                                                                                          Cell adhesion;
REPEAT 157
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SEQUENCE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                         Y787_SYNY3
Q55946;
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                   REPEAT
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 868;
                                                                                                                                                                                                                                               15-Jūr-1998 (Rel. 36; Created)
15-Jūr-1998 (Rel. 36; Last sequence update)
16-CCT-2001 (Rel. 40; Last annotation update)
Aconitate hydratase 2 (EC 4.2.1.3) (Citrate hydro-lyase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON (IRON-SULFUR CLUSTER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
EBF93B0F966A94EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyase, Tricarboxylic acid cycle; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                      11;
                                                                                                 210 REDVSMGGTGTALMILETSKCGAILDLDAISCPAGL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                              TROEGMEGILGTLYQLLGSD-----DINVVTCAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.1%; Score 54.5; 38.5%; Pred. No. 15;
Score 56; DB Pred. No. 3.7;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Problem, PD000511; Aconitase; 1.
PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         868 AA; 93551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D90916; BAA18689.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphohydroxypyruvate + NaDH.
EN2YME REGULATION: IN BACTERIA DISPLAYS FEEDBACK INHIBITION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- PATHWAY: FIRST COMMITTED STEP IN THE "PHOSPHORYLATED" PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=168 / MARBURG;
MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID
DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
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Oxidoreductase; NAD; Complete proteome.

Sy SUBSTRATE-BINDING (BY SIMILARITY BY SIMILARITY BY SIMILARITY BY SIMILARITY CAS BY SIMILARITY CAS BY SIMILARITY.

57115 MW; B3D0854487DD44FF CRC64;
                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (PGDH).
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
525 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00065; D_2_HYDROXYACID_DH_1; 1.
PROSITE; PS00670; D_2_HYDROXYACID_DH_2; 1.
PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
Serine biosynthesis; Oxidoreductase; NAD; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002912; ACT.
InterPro; IPR002162; D_2_hydroxyacid_DH.
Pfam; PF00389; 2-Hacid_DH; 1.
Pfam; PF02826; 2-Hacid_DH_C; 1.
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 107-525 FROM N.A.
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EMBL; Z99116; CAB14239.1; -.
EMBL; L09228; AAA67502.1; -.
HSSP; P33160; ZNAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SubtiList; BG10509; serA.
                                                                                                                                                                              STANDARD;
                                                                                                                                                                        SERA_BACSU STANDARD
P35136; O32011;
01-FEB-1994 (Rel. 28, C
15-UUL-1998 (Rel. 36, L
16-OCT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARBURG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-SERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serror P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
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 Gaps
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 MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyalima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.
Shimpo S., Takeuchi C:, Wada T., Watanabe A., Yamada M., Yasuda M.,
 Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
 "Sequence analysis of the genome of the unicellular cyanobacterium
 : phosphohydroxypyruvate + NADH.
 PRGSITE; PRO0065; D.2_HYDROXYACID_DH_1; 1.
PRGSITE; PSO0670; D.2_HYDROXYACID_DH_2; 1.
PRGSITE; PSO0671; D.2_HYDROXYACID_DH_3; 1.
Serine biosynthesis; Oxidoreductase; NAD; Complete protecome.
ACT SITE 258 SUBSIRATE-BINDING (BY SIMILARITY).
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 -1- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID
 DB 1; Length 554;
16;
 DB 1; Length 525
 Indels
 16#OCT-2001 (Rel. 40, Last annotation update)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (PGDH).
 -!- CATALYTIC ACTIVITY: 3-phosphoglycerate + NAD(+) = 3-
 1D25DCDE7A8DB1D9 CRC64;
 Bacteria; Cyanobacteria; Chroococcales; Synechocystis. NCBI_TaxID=1148;
 13;
 (Rel. 36, Created)
(Rel. 36, Last sequence update)
 7; Mismatches
 SIMILARITY
SIMILARITY
 Mismatches
 Interpro; IPR002912; ACT.
Interpro; IPR002162; D.2_hydroxyacid_DH.
Interpro; IPR00316; D.2_hydroxyacid_DH.
Pfam; PP00389; 2-Hacid_DH; 1.
Pfam; PF03826; 2-Hacid_DH_C; 1.
Pfam; PF01842; ACT; 1.
Match ...27.8%; Score 54; Local Similarity 39.1%; Pred. No. 1
 11arity 33.3%; Score 53; Conservative 7; Mismatcl
 3 TKQEGMEGLLGTLVQLLGSDDINVVTCAAG 32
 Synechocystis sp. (strain PCC 6803)
 462 GVIGRVGRILGDNDINIATMQVG 484
 10 GLLGTLVQLLGSDDINVVTCAAG 32
 59221 MW;
 OF L-SERINE BIOSYNTHESIS
 EMBL; D90910; BAA17878.1; -. HSSP; P08328; 1PSD.
 DEHYDROGENASES FAMILY.
 Conservative
 STANDARD;
 3:109-136(1996).
 SEQUENCE FROM N.A.
 Query,Match
Best^{or}Local Similarity
Matches (10) Conserv
 SERA OR SLL1908
 15-JUL-1998
16-OCT-2001
 15:JUL-1998
 SERA_SYNY3
P73821;
 Query, Match
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 SERA_SYNY3
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485 TLHRDMPGIIGKIGSLLGSFNVNIASMQVG 514

Search completed: July 29, 2002, 16:09:55 Job time: 760 sec

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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068870 hepatitis c
09920 caulobacter
09920 caulobacter
09926 schizosacch
091487 hepatitis c
09006 schizosacch
049659 arabidopsis
081495 hepatitis c
091495 hepatitis c
091769 bacillus su
092763 rhizoblum m
09689 paenibacill
094203 mus musculu
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095169 arabidopsis
091697 arabidopsis
091697 arabidopsis
09600 hepatitis c
068801 hepatitis c
068801 hepatitis c
099905 drosophila
098705 drosophila
098705 drosophila
Q81258 hepatitis c
 axis in zebrafish occurs following
 Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
 Length
 Indels
 ARM_REPEAT; 8.
; 85542 MW; D7A1FB80F94066DC CRC64;
 1.NOV-1996 (TrEMBLrel. 01, Created)
1.NOV-1996 (TrEMBLrel. 01, Last sequence update)
1.DEC-2001 (TrEMBLrel. 19, Last annotation update)
 100.0%; Score 194; DB 13;
nilarity 100.0%; Pred. No. 4.6e-18;
Conservative 0; Mismatches 0;
 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 780 AA
 ALIGNMENTS
 MEDLINE-96122902; PubMed-8562427; Kelly G.M., Erezyilmaz D.F., Moon R.T.; Induction of a secondary embryonic axis the overexpression of beta-catenin."; Mech. 50ev. 53:261-273(1995) EMRL; U41081; AAC59732.1; HSSP; P35222; 1G3J.
 099WIB
06870
094302
094302
094305
091406
099UT06
091495
091495
091783
096203
096203
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096203
096203
096203
09769
 Q9FYA4
Q9FTH3
Q95PH6
O92530
Q68801
Q9V905
Q98RP2
O52072
 ZFIN; ZDB-GENE-980526-362; ctnnb.
InterPro; IPR000225; Armadillo.
Pfam; PF00144; Armadillo.seg; 12.
SMART; SM0185; ARM; 111.
PROSITE; PS50176; ARM; REPEAT; 8.
SEQUENCE 780 AA; 85542 MW; D7A
 100
100
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100
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100
100
 12
 PRELIMINARY;
 2062
3013
3019
465
 Local Similarity
ès 39; Conserv
 SEQUENCE FROM N.A.
 NCFI_TaxID=7955;
 01-NOV-1996
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 Q9d335 mus muscull
Q42486 gallus gall
Q25100 hydra magni
Q9pvf7 brachydanio
Q9n144 ciona intes
O76152 ciona savig
Q15151 homo sapien
Q9bwc4 homo sapien
 P70565 rattus norv
061229 lytechinus
044326 caenorhabdi
010953 caenorhabdi
049300 arabidopsis
001596 pneumocysti
092933 hepatitis c
 090424 brachydanio
 (without alignments)
54.235 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 July 29, 2002, 16:12:07; Search time 124.4 Seconds
 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC
 4.5
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 562222 seqs, 172994929 residues
 SUMMARIES
 GenCore version
Copyright (c) 1993 - 2000
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 090424
090335
042486
025100
09FVF7
090154
076152
096122
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
 sp_unclassified:*
 sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
 sp_bacteriap:*
 sp_organelle:*
sp_phage:*
 US-09-641-104A-10
 seq length: 0 seq length: 2000000000
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 sp_rvirus:*
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 SPTREMBL_19:*
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 sp_mhc:*
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 Query
Match 1
 100.0
77.3
74.7
74.2
74.2
74.2
66.0
66.0
66.0
64.3
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Pred. No.

Score

Result No.

1994 1944 1944 1128 1128 1120 711 62 62 63

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RESULT 090335

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Hydra magnipapillata (Hydra).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
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 MEDLINE-96257271; PubMed-8654977;
Hobmayer E., Hatta M., Fischer R., Fujisawa T., Holstein T.W.,
Sugiyama T.;
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 Length 781;
 Length 806;
SEQUENCE FROM N.A.; TISSUE-DORSAL SKIN; STRAIN-WHITE LEGHORN; TISSUE-DORSAL SKIN; STRAIN-WHITE LEGHORN; TISSUE-DORSAL SKIN; LUAT, Chuong C.M.; Widelitz R.B.; "Képlation and C.M.; Widelitz R.B.; "Képlation and Characterization of chicken beta-catenin."; General 196:201-207(1997).
 Indels
 Indels
 InterPro; TR000225; Armadillo.
Pfam: PF00514; Armadillo_seg; 10.
SMART; SM00185; ARM; 10.
PROSITE; P50176; ARM_REBAT; 7.
PROSITE: 806.AA; 90462 MW; 689E5E982CD5051A CRC64;
 01:MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL-ADHESION PROTEIN PLAKOGLOBIN.
 Last sequence update)
Last annotation update)
 "Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadillo gene family.";
 Score 194; DB 13;
Pred. No. 4.6e-18;
 ö
 351 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 429
 Query Match 77.3%; Score 150; DB 5; Best.Local Similarity '76.3%; Pred. No. 5.1e-12; Matches 29; Conservative 5; Mismatches 4
 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 Brachydanio rerio (Zebrafish) (Zebra danio).
 729 AA
 806 AA
 Mismatches
 Created)
 PRT;
 PRT;
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 Match
Local Similarity, 100.0%;
 Gene 172:155-159(1996).
EMPL; (U36781; AAC47137.1; -.
HSSP; Q02248; 2BCT.
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
 Matches, 29; Conservative
 39; Conservative
 PRELIMINARY;
 PRELIMINARY;
 806 .AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=6085;
 BETA-CATENIN.
 SEQUENCE
 Query Match
 Q25100
Q25100;
 Q9PVF7;
 Q9EVE7
 RESULT; 5 5 0
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 Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Ra Gato T., Davis S., Matsuo T., Gissi C., King B., Kochiwa H.,
Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ra Baka J., Boffelli D., Bojiuga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Anchionni L., Mashima J., Mazarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Anachizaki Y.
 ö
 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Functional annotation of a full-length mouse cDNA collection.";
 0;
 Length 781;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last senotation update)
ADULT MALE COLON CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 9030417H18, FULL INSERT SEQUENCE.
 Indels
 SM00185; ARM; 12.
2; PSS0176; ARM_REPEAT; 7.
2E 781 AA; 85546 MW; 937538C3B5CD75D1 CRC64;
 Last sequence update)
Last annotation update)
 100.0%; Score 194; DB 11; 100.0%; Pred. No. 4.6e-18;
 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 781 AA.
 781 AA.
 0; Mismatches
 Created)
 PRT;
 PRT;
 STRAIN-C57BL/6J; TISSUE-COLON;
MEDLINE-21085660; PubMed-11217851;
 MGD; MGI:88276; Catnb.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
 Nature 409:685-690(2001).
EMBL; AK018515; BAB31250.1; -.
 042486 PRELIMINARY;
042486;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
 Conservative
 PRELIMINARY;
 Mus musculus (Mouse)
 Query Match
Best Local Similarity
Matches 39; Conserv
 HSSP; P35222; 1G3J
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Gallus.
NCBI_TaxID=9031;
[1]
 Hayashizaki Y.;
 BETA CATENIN.
 PROSITE;
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 Q9D335;
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Gaps

RESULT 042486

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TISSUE=PLACENTA;
MEDLINE=96157724; PubMed=8576101;
Ozawa M., Nuruki K., Toyoyama H., Ohi Y.;
"Cloning of an alternative form of plakoglobin (gamma-catenin) lacking
 Cióna, savignyl!
Eukaryota; Metázoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Ciónidae; Cioná.
 Schiller D.L., Cowin P.; "Molecular cloning and amino acid sequence of human plakoglobin, the
 MEDINE-98443204; PubMed-9769178; Yoshida S., Marikawa Y., Satoh N.; Negolation of the trunk-tail patterning in the ascidian embryo: a possible interaction of cascades between lithium/beta-catenin and localized maternal factor pem."; Dev. Biol. 202:264-279(1998).
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SEQUENCE FROM N.A. PubMed=1101683-1101
 SECTENCE FROM N.A.
MEDLINE-89264555; PubMed-2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
 Length 773;
 Indels
 Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
 nicerpo; IPR000225; Armadillo.
Pfam: PF00514: Armadillo_seg; 11.
SMART: SM00185; ARM; PEPEAT; 7.
SEQUENCE 773 AA; 85217 MW; C1340CF82AFEBDAB CRC64;
 Last sequence update)
Last annotation update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
 common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989)
 Query Match 74.2%; Score 144; DB 5; Best Local Similarity 76.9%; Pred. No. 3.2e-11; Matches 30; Conservative 3; Mismatches 6;
 390 AGTKQDQVENLLQMLVQLLSSNDINVVTCAAGILSNLTC 418
 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 745 AA.
 Created)
 Exp. Dermatol. 9:323-326(2000).
EMBL; Z68228; CAA92522.1; -.
 the fourth armadillo repeat."; J. Biochem. 118:836-840(1995).
 015151 PRELIMINARY;
015151; 015093;
01.000-1996 (TEMBLEEL. 01, C:
01-NOV-1996 (TEMBLEEL. 01, Le
01-JUN-2001 (TEMBLEEL. 17, Le
PLAKOGLOBIN.
 SEQUENCE OF 239-409 FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 HSSP; P35222; 1G3J
 NCBI_TaxID=51511;
 NCBI_TaxID=9606;
 Zimbelmann R.;
 BETA-CATENIN.
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 Ciona intestinalis.
Eukaryota, Metazoa; Chordata, Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona.
NCBI_TaxID=7719;
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 SEQUENCE FROM N.A.
MEDILTE=99386700; PEAGE S., Franke W.W.;
"Cerda J., Reidenbach S., Pratzel S., Franke W.W.;
"Cadherin-catenin complexes during zebrafish oogenesis: heterotypic junctions between cocytes and follicle cells.";
Biol. Reprod. 61:692-704(1999).
EMBL; AF099738; AADS6592.1; -.
 SEQUENCE FROM N.A. Imai K., Takada N., Satou Y.; Imai K., Takada N., Satoh N., Saton Y.; "An essential role of beta-catenin in the endoderm specification of
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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 Length 729;
 74.2%; Score 144; DB 5; Length 769; ilarity 76.9%; Pred. No. 3.2e-11; Conservative 3; Mismatches 6; Indels
 Indels
 Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases EMBL; AB031543; BAA92185.1; -.
 InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; II.
PROSITE; PS0176; ARM; REPEAT; 6.
SEQUENCE 769 AA; 84703 MW; F61CC489B436E1BC CRC64;
 91E00417B4FD8CEE CRC64;
 Last sequence update)
Last annotation update)
 Created)
Last sequence update)
 9
 74.7%; Score 145; DB 13;
71.8%; Pred. No. 2.2e-11;
 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 1 AATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 769 AA
 5; Mismatches
 EMBL; AF099, 20, ...
HSSP; Q02248; IDOW.
ZFIN; ZDB-GENE-991207-22; jup.
InterPro; IPRO00225; Armadillo.
Pfam; PRO014; Armadillo.seg; 11.
RMART; SM01185; ARM; 8.
PROSITE; PS50176; ARM_REPEAT; 8.
 Created)
 PRT;
 PRT;
 076152 PRELIMINARY;
076152;
01-NOV-1998 (TrEMBLEEL: 08, 01-NOV-1998 (TrEMBLEEL: 08, 01-NOV-1998)
 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
 Conservative
 PRELIMINARY;
 Query Match
Best Local Similarity
Matches 28; Conserv
 Query Match
Best Local Similarity
Matches 30; Conserv
 HSSP; P35222; 1G3J
 ascidian embryo.";
 NCBI_TaxID=7955
 BETA-CATENIN.
CIBETA-CATENIN
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RESULT Q9NL44

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MEDITME-98104237; PubMed-9441670; MAILE JR., McClay D.R.; McClay D.R.; McClay D.R.; Miller J.R., McClay D.R.; Miller J.R., McClay D.R.; Mailer J.R., McClay D.R.; Mailer J.R.; McClay D.R.; Dev.; McChaiges in the pattern of adherens junction-associated beta-catenin accompany morphogenesis in the sea urchin embryo."; Dev. Biol. 192:310-322(1997). McClosub 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
BETA-CATENIN.
Lytechinus variegatus (Sea urchin.
Eukaryota: Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinodermata; Temnopleuroida; Toxopneustidae;
 Umekita Y., Liao S.;
"Molecular cloning and sequencing of the rat plakoglobin cDNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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 Length 745;
 Length 821;
 6; Indels
 Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U58858; AAB06317.1; -- HSSP; Q002248; 2BCT.
 InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR00225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SWART; SW00185; ARW; 12.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_I.
PROSITE; PS00176; ARW_REPEAT; 8.
 InterPro: IPR00225; Armadillo.
Pfam: PF00514; Armadillo_seg; 11.
SMART: SM00185; ARM; 8P
PROSITE: PS50176; ARM_REPEAT; 7.
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 64.9%; Score 126; DB 11;
65.8%; Pred. No. 9.2e-09;
Live 4; Mismatches 9;
 Ouery Match
Best Local Similarity 73.5%; Pred. No. 6.8e-08;
Matches 25; Conservative 3; Mismatches 6;
 383 ATKQEGLENVLKILVNQLSVDDVNVLTCATGHLSNLTC 420
 . 2 ATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 413 DDIEPLLQMLVQLLASNDINVVTCACGILSNLTC 446
 678 AA
 6 EGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
 SEQUENCE FROM N.A. STRAIN-SPRAGUE-VAGINA;
 STRAIN-SPRAGUE DAWLEY; TISSUE-VAGINA;
 PRT;
 Query Match
Best Local Similarity 65.8°
Matches 25; Conservative
 PRELIMINARY;
 PRELIMINARY;
 NCBI_TaxID=7654;
 SEQUENCE FROM N.A.
 Hiipakka R.A.
 Lytechinus
 RESULT 12
044326
ID 044326
AC 044326
 061229
 RESULT 11
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 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 Gaps
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Length 745;
 Length 745;
 Indels
 Indels
 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC000441; AMH00441.1; -.
EMBL; BC010465; AAH11865.1; -.
HSSP; O02248; 2BCT.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo.seg; 11.
SMART; SMO0185; ARM; 12.
PROSITE; PS50176; ARM_REPEAT; 7.
 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 745 AA; 81726 MW; 34DF7BFB4748BCF4 CRC64;
 3519A0973748BCF4 CRC64;
 Last sequence update)
Last annotation update)
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
JUNCTION PLAKOGLOBIN.
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 Query Match 66.0%; Score 128; DB 4; Best Local Similarity 65.8%; Pred. No. 4.9e-09; Matches 25; Conservative 4; Mismatches 9;
 383 ATKQEGLESVLKILVNQLSVDDVNVLTCATGTLSNLTC 420
 383 ATKQEGLESVLKILVNQLSVDDVNVLTCATGTLSNLTC 420
 2 ATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTC 39
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 745 AA.
 745 AA.
 Created)
 PRT;
 EMBL; AF3306723; AAG16727.1; -.
EMBL; AF233882; AAG16727.1; JOINED.
 PRT;
 HSSP; Q02248; ZBCT.
InterPro; IPR000225; Armadillo.
Pfam; PF00014; Armadillo_seg; 11.
SMART; SM00185; ARM; 9.
PROSITE; PS50176; ARM, REPEAT; 7.
SEQUENCE 745 AA; 81744 MW; 35
 SEQUENCE FROM N.A.
TISSUE-PLACENTA, CHORIOCARCINOMA;
D50808; BAA09435.1; -.
 01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19, PLAKOGLOBIN.
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
TISSUE-LUNG CARCINOMA;
 Homo sapiens (Human)
 NCBI_TaxID=10116;
 NCBI_TaxID-9606;
 SEQUENCE
 P70565
P70565;
 Q9BWC4
 RESULT 10
 RESULT
 Q9BWC4
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Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
 SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;

Pederspiel N.A., Pallm C.J., Conway A.B., Kurtz D.B., Conway A.R.,

Pederspiel N.A., Pallm C.J., Conway A.B., Kurtz D.B., Conway A.R.,

Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,

Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S.,

Yu G., Ecker J., Theologis A., Davis R.W.;

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AC002311; AAC006021:

InterPro; IPR00025; Armadillo.

Pram: PPROSIL: PARMATEPEAT; 4.

SWART; SM00185; ARM, 5.

SEQUENCE 1299 AA; 142073 MW; 08C200BDF7D0B82F CRC64;
 Ali M., Priess J.R., Mello C.C.;
"Mnt: signaling and an APC-related gene specify endoderm in early C. elegans embryos ":
Cell.90:707-716(1997):
 Length 1299;
 Ouery Match 33.0%; Score 64; DB 5; Length 796; Best Local Similarity 33.3%; Pred. No. 3.1; Matches 12; Conservative 10; Mismatches 14; Indels
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 EMBL; U32305; AAK18863.1; -.
EMBL; AF013951; AAC47748.1; -.
InterPro; IPR000225; Armadillo.
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 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 Last sequence update)
Last annotation update)
 10;
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 454 AIQEQDMKEŠIHCIVQLIGCSDVTIVELATGTLRNI 489
 2 ATKOEGMEGLLGTLVQLLGSDDINVVTCAAGILSNL 37
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 11 · ELGTLVQLLGSDDINVVTCAAGILSNL 37
 PRT;
 01:NOV-1996 (TrEMBLrel. 01, 01, NOV-1998 (TrEMBLrel. 08,
 01-NOV-1996 (TrEMBLrel. 01,
 GLYCOPROTEIN A (FRAGMENT).
Pneumocystis carinii.
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 T26J12.6 PROTEIN.
 NCBI_TaxID=4754;
 NCBI_TaxID=3702;
 Pneumocystis
 T26J12.6.
 049300;
 001596
 001596;
 049300
 RESULT .14
 RESULT
Q01596
 049300
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 Gaps
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
 STRAIN=BRISTOL;
MEDLINE-97433081; PubMed-9288750;
Rocheleau C.E., Downs W.D., Lin R., Wittmann C., Bei Y., Cha Y.-H.,
 ö
 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
 36.6%; Score 71; DB 5; Length 678, 35.9%; Pred. No. 0.29; Live 10; Mismatches 15; Indels
 [1]
SEQUENCE FROM N.A.
STRAIN-N2 BRISTOL;
Costa M., Raich W., Agbunag C., Hardin J., Priess J.R.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
 "The sequence of C. elegans cosmid B0336.";
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
 to the EMBL/GenBank/DDBJ databases
 to the EMBL/GenBank/DDBJ databases
 Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 6.
PROSITE; PS50176; ARM_REPEAT; 1.
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Last sequence update)
Last annotation update)
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2011 (TrEMBLrel. 17, La
B0336.1 PROTEIN (WRW-1).
B0336.1 OK WRW-1.
 Submitted (NOV-1996) to the EM
EMBL; AR016653; AAB94552.1; -.
EMBL; Z81564; CAB04572.1; -.
HSSP; P35222; 1G37.
01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
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Caenorhabditis elegans.
 Submitted (MAR-2001)
 Best Local Similarity
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 STRAIN-BRISTOL N2;
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 SEQUENCE FROM N.A.
 NCBI_TaxID=6239;
 Waterston R.
 Harris B.:
 Taich A.;
 Query Match
 010953
 Matches
 RESULT
Q10953
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Gaps

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RC STRAIN-C.B-17 SCID/SCID MOUSE-DERIVED PNEUMOCYSTIS CARINII;
RA WIGHT TW. Simpson-Haidaris P.J., Gigliotti F., Harmsen A.G.,
RA Haidaris C.G.;
RT "Conserved sequence homology of cysteine-rich regions in genes
renceding glycoprotein A in Pneumocystis carinii derived from different
RT host species.";
RL Infect. Immun. 62:1513-1519(1994).
BEBEL; U5262; AAA18864.1; -.
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SQUENCE 103 AA; 12128 MW; B7AA05EE826438B5 CRC64;
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Search completed: July 29, 2002, 16:12:09 Job time: 479 sec

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 16:07:56; Search time 158.47 Seconds Run on:

(without alignments)
30.840 Million cell updates/sec

US-09-641-104A-11 227 Title: Perfect score: Sequence:

1 NNYKNKMMVCQVGGIEALVR.....AGDREDITEPAICALRHLTS

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*
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22: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:\* 2200 ..... 2200 ..... 2200 ..... 2200 ..... 2200 ..... 2200 ....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|        | Description     | Human beta-catenin | Human beta catenin | Human beta-catenin | Novel human secret | Human beta-catenin | Mouse beta-catenin | Human beta-catenin | Drosophila melanog | Drosophila melanog | Drosophila melanog | Human prostate can |
|--------|-----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|        | ΩI              | AAY33222           | AAB07290           | AAY70740           | AAU28118           | AAE06038           | AAE06039           | AAY33237           | ABB60196           | ABB65819           | ABB65821           | AAB56810           |
|        |                 | 20                 | 21                 | 21                 | 22                 | 22                 | 22                 | 20                 | 22                 | 22                 | 22                 | 21                 |
|        | Match Length DB | 44                 | 781                | 781                | 781                | 781                | 781                | 44                 | 840                | 840                | 840                | 345                |
| Query  | Match           | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 99.1               | 82.4               | 82.4               | 82.4               | 73.1               |
|        | Score           | 227                | 227                | 227                | 227                | 227                | 227                | 225                | 187                | 187                | 187                | 166                |
| Result | No.             | 1                  | 7                  | m                  | 4                  | S                  | 9                  | 7                  | 80                 | 6                  | 10                 | 11                 |

| .l.rag | بدة          |             | :     |    |            | Page 1             |
|--------|--------------|-------------|-------|----|------------|--------------------|
|        |              |             |       |    |            |                    |
|        | ·-:          | <del></del> |       |    |            |                    |
|        | : - <b>.</b> |             |       |    |            |                    |
| 12     | 1166         | 73:1        | 100   | 12 | AAR11354   | Cellular Receptor  |
| 13     | 11           | ~           | 800   | 22 | AAU28306   | Novel human secret |
| 14     | 58.          | 25.8        | 797   | 21 | AAB36462   | plakophi           |
| 15     | œ.           | S           | 797   | 22 | AAM79226   | Human protein SEQ  |
| 16,    | 58.5         | ď.          | , 817 | 22 | AAM80210   | Human protein SEQ  |
| 17     | 7.           | 2           | . 531 | 22 | ABG00802   | Novel human diagno |
| 18.    | n.           | S.          | 160   | 21 | AAG14043   | 13                 |
| 19.5   |              | 2           | : 161 | 21 | AAG39419   | O)                 |
| 50     | 57           | S           | 164   | 21 | AAG14042   | is                 |
| 21;    | . 3 57       | S           | 1.165 | 21 | AAG39418   | is                 |
| 22 7   | S            | S           | 178   | 21 | AAG14041   | S                  |
| -      | . 5          | S           | 206   | 21 |            | Arabidopsis thalia |
| 24     | 55.          | 24.4        | 223   | 21 |            | Corn beta-carotene |
| 25,    | 4            | 4           | 978   | 22 |            | Staphylococcus aur |
| 56     | 54.5         | 24.0        | 1:987 | 22 | AAU36599   | Staphylococcus aur |
| 27,    | S            | 3           | 1106  | 22 | AAU03552   | Human protein kina |
| 28     | ä            | $^{\circ}$  | 686   | 22 | AAE10797   | -                  |
| 53     | S            | <br>        | 461   | 21 | AAG36942   | s                  |
| 30     | S            |             | 480   | 21 | AAG36941   |                    |
| 31     |              | ά.          | 564   | 21 | AAG36940 . | Arabidopsis thalia |
| 32     | •            | ς.          | 201   | 22 | AAU40279   | Propionibacterium  |
| 33     | ij.          | 2           | 267   | 22 | AA009551   | Human polypeptide  |
| 34.    | ij.          | ς.          | 197   | 21 | AAB36466   | Mouse plakophilin- |
| 35     | S            | 2           | 191   | 21 |            | Neisseria meningit |
| 36 .   | , 51         | 22.5        | 775   | 22 | ABB60574   | Drosophila melanog |
| 37 .   | . 51         | 2           | 1009  | 22 | ABG20820   | Novel human diagno |
| 38     | 51           | ~           | 1110  | 22 | AAE03648   | Human extracellula |
| 39     | . 51         | 5           | 1192  | 20 | AAY23899   | Human resenilin bi |
| 40     | 51           | ä           | 1211  | 18 | AAW24560   | -int               |
| 41     | . 51         | 22:5        | 1211  | 21 | AAY92336   |                    |
| 42     | 51           | á           | 1445  | 12 | AAR12108   |                    |
| 43     | . 51         | ď.          | .1522 | 10 | AAP93357   | Sequence of the ca |
| . 44   | . 51         | 22.5        | 1644  | 18 | AAW13504   | B. bronchiseptica  |
| 45     | . 51         | 22.5        | 1645  | 18 | _          | B. pertussis adeny |

### ALIGNMENTS

AAY33222 standard; peptide; 44 AA. 

(first entry) 18-NOV-1999

AAY33222;

Human' beta-catenin protein armadillo repeat arm8 fragment.

Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor'suppressor gene; conductin; B-cadherin; screening; carcinoma; APC; Wnt signalling pathway; tumor development; anti-oncogenic; melanoma; organ regeneration; tissue regeneration; hair growth

Homo sapiens.

DE19909251-A1.

26-AUG-1999.

99DE-1009251 22:FEB-1999; 21-FEB-1998; · 98DE-1007390

(DELB:) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

Birchineier W, Von Kries J;

WPI; 1999-470389/40.:

Agents for treating human diseases, particularly cancer, modulate interaction of beta-catenin with transcription factors or tumor

.

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This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or specific interaction of mimunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin (E) as key compound in the Wht signalling pathway and is involved in development of tumors. Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is concepting the interaction and melanoma, but also, treat tumors, especially carcinoma of the colon and melanoma, but also, the catenin armadillo repeat fragments described in the method of the
 New antisense compounds targeting nucleic acids encoding human beta catenin (HBC) useful for treating diseases associated with HBC expression and as prophylaxis to prevent or delay infection, inflammation or tumor formation
 itenin; cadherin; metastasis; cadherin-associated protein;
colorectal cancer; melanoma; antisense oligonucleotide;
 ;
0
 Length 44;
 Indels
 44
 44
 1 nnyknkmmvcqvggiealvrtvlragdreditepaicalrhlts
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 100.0%; Score 227; DB 20;
ilarity 100.0%; Pred. No. 3.4e-26;
Conservative 0; Mismatches 0;
 AAB07290 standard; Protein; 781 AA
 Disclosure; Page 7; 16pp; German.
 99US-0344519
 99US-0344519
 (first entry)
suppressor gene products
 Cowsert LM;
 (ISIS-) ISIS PHARM INC.
 WPI; 2000-410651/35.
 Query Match
Best Local Similarity
Matches 44; Conserv
 Human beta catenin.
 N-PSDB; AAA58320.
 44 AA;
 catenin;
 human; colore
gene therapy.
 Homo sapiens
 25-JUN-1999;
 25-JUN-1999;
 01-NOV-2000
 Bennett CF,
 JS6066500-A
 23-MAY-2000
 AAB07290;
 Sequence
 AAB07290
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 The patent discloses a method of female primate contraception comprising administering an antagonist of a Wnt polypeptide, inhibiting oocyte development. Wnt polypeptides are useful for promotive meturation of an immature occyte. Wnt polypeptides are also useful for increasing the number of mature occytes and to enhance occyte viability. Soluble fragments of Wnt polypeptides have the ability to inhibit Wnt signalling, e.g., by blocking binding of a naturally-occurring Wnt protein to its receptor. They may be used to generate monoclonal antibodies which can inhibit occyte development. The present sequence is the human beta-catenin protein. Dominant negative mutants of beta-catenin lack one
 Human, beta-catenin; Wht antagonist; contraceptive; contraceptive vaccine; oocyte development; female primate contraception; oocyte viability; monoclonal antibody; Wht signalling.
 Retarget catenin is a member of the catenin family of cytosolic proteins and a key member of the Wnt signalling pathway. Catenins interact with the cytoplasmic domains of cadherin glycoproteins, and are important in maintaining cell adhesiveness. The loss of cell adhesiveness is implicated in metastasis. Bete catenin is also known as cacherin-associated protein and is implicated in colorectal cancer and melanoma. The present sequence is the human beta catenin protein. The coding sequence of this protein was used in the present invention to design antisense oligonucleotides (AAA58127-A58366). The oligonucleotides are capable of hybridising to human beta catenin, in order to inhibit expression of human beta catenin. The oligonucleotides may be used in gene: therapy for colorectal cancer or melanoma.
 Contraceptive composition for inhibiting oocyte development in a female
 Gaps
 ;
0
 Length 781;
 Indels
 44
 430 nnyknkmmvcqvggiealvrtvlragdreditepaicalrhlts
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Ouery Match 100.0%; Score 227; DB 21; Best Local Similarity 100.0%; Pred. No. 9.6e-25; Matches 44; Conservative 0; Mismatches 0;
 primate comprises a Wnt polypeptide antagonist
 Example 13; Columns 45-52; 35pp; English.
 AAY70740 standard; protein; 781 AA
 Example 3; Page 26; 57pp; English.
 Mcmahón AP, Parr BA, Vaino S;
 99WO-US23640.
 · 98US-0104355.
 24.JUL-2000 (first entry)
 (HARD':) HARVARD COLLEGE.
 WPI; 2000-317845/27.
 Human beta-catenin.
 Beta catenin is
a key member of
 WO200021555-A1.
 Homo sapiens.
 13-0cm-1999;
 15-0ch-1998;
 20 APR-2000.
 AAY70740;
 Seguence
 AAY70740
 RESULT
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Gaps

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 The invention relates to novel isolated human secreted polypeptides (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, isolaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (I) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of
 <u>.</u>
۵
 Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
or more armidillo-like repeats which participate in cadherin binding. Other mutants include those lacking amino acids 555-781 or 424-781, or 1-422 of beta-catenin.
 Gaps
 n F, Ma Y, Zhou
Xue AJ, Wang J;
 Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
 ő
 Length 781;
 Indels
 Xu C, Wehrman T, Ren F,
T, Zhang J, Chen R, Xue
 NNYKNKMWVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
 0%; Score 227; DB 21;
0%; Pred. No. 9.6e-25;
0; Mismatches 0;
 Novel human secretory protein, Seq ID No 287.
 Example 4; SEQ ID No 287; 107pp; English.
 Ş
 AAU28118 standard; Protein; 781
 Liu C, Asundi V, Xu
Yang Y, Drmanac RT,
 100.0%;
100.0%;
 2000US-0519705.
2000US-0574454.
2000US-0596193.
2000US-0616847.
2000US-0665363.
 05-MAR-2001; 2001WO-US04942
 2000US-0693267
 (first entry)
 Conservative
 WPI; 2001-589934/66.
 Similarity
 781 AA;
 (HYSE-) HYSEQ INC.
 N-PSDB; AAS45018
 WO200166689-A2.
 Homo sapiens.
 20-OCT-2000;
 07-MAR-2000;
 19-MAY-2000;
17-JUN-2000;
 14-JUL-2000;
 19-SEP-2000;
 Query Match
Best Local Simi
Matches 44;
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 13-SEP-2001
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 rang YT,
 Zhao QA,
 Sequence
 430
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 AAU28118
 RESULT
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The Portype pulse as well as too studying modurators of the proliferation of neural cells and regeneration of nerve and brain tissue and its useful for the treatment of central and perhaps and its useful for the treatment of central and perhaps and its user and such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral activity, regulation of haematcopiesis and is useful for treating myeloid or champer and its useful for treating myeloid or lissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (1) is also useful for quiptotection or regeneration and treatment of lung or liver fibrosis, reperfusion Injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or füngal infections, autoimmune disorders e.g. multiple sclerosis, cheumatcid arthritis, and abeliam systhenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects blorhythms or circadian cycles of rhythms, allergic activities and conditions and problems, anabolism, anabolism, storage or elimination of
 ö
 dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analyssic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein
 In vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of beta-catenin in the cell
polypeptide as well as for studying modulators of the polypeptides.
 Human; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient;
 Gaps
 ;
0
 Length 781;
 Indels
 44
 430 nnyknkmmvcqvggiealvrtvlragdreditepaicalrhlts
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 100.0%; Score 227; DB 22;
100.0%; Pred. No. 9.6e-25;
tive 0; Mismatches 0;
 amino acid sequences of the invention.
 (ST'RD) UNIV LELAND STANFORD JUNIOR.
 AAE06038 standard; Protein; 781 AA
 signalling pathway; beta-catenin.
 Human beta-catenin protein #1.
 17-JAN-2001; 2001WO-US01459.
 2000US-0176786.
 Reya T, Nusse R, Weissman
 (first entry)
 Best Local Similarity 100.
Matches 44; Conservative
 WPT; 72001-465328/50.
 781 AA;
 N-PSDB; AAD11164.
 WC200152649-A1:
 Homo sapiens. .
 26-JUL-2001.
 18-JAN-2000;
 25-SEP-2001
 Sequence
 AAE06038;
 Query Match
 RESULT . 5
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Page 23-24; 33pp; English.
 processes
\mathbf{x} \overset{\mathsf{x}}{\mathbf{x}} \overset{\mathsf{x}}{\mathbf{x}} \overset{\mathsf{y}}{\mathbf{y}} \overset{\mathsf{y}}{\mathbf{y}} \overset{\mathsf{y}}{\mathbf{y}} \overset{\mathsf{y}}{\mathbf{y}} \overset{\mathsf{y}}{\mathbf{y}}} \overset{\mathsf{y}}{\mathbf{y}} \overset{\mathsf{y}}
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The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell in an in vitro culture medium for a period sufficient for the progenitor or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells having the functional useful for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or the contraction is a source of stem cells. transplantation to restore haematopoietic function to autologous or allogeneic recipients. The present sequence is human betta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway initiated by Wnt proteins, which are mediators of several developmental

781 AA; Sequence

Gaps ö Length 781; Indels 44 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS Score 227; DB 22; Pred. No. 9.6e-25; Mismatches ; 0 100.08; 100.0%; Conservative Best Local Similarity 44; Query Match Matches ò

430 nnyknkmmvcqvggiealvrtvlragdreditepaicalrhlts 473

9

AAE06039 standard; Protein; 781 AA AAE06039

25-SEP-2001 (first entry)

Mouse beta-catenin protein #2.

Mouse; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient; signalling pathway; beta-catenin. 

Mus musculus.

WO200152649-A1.

26-JUL-2001

17-JAN-2001; 2001WO-US01459

(STRD ) UNIV LELAND STANFORD JUNIOR.

18-JAN-2000; 2000US-0176786

Reya T, Nusse R, Weissman IL;

WPI; 2001-465328/50. N-PSDB; AAD11165.

In vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of beta-catenin in the cell

Disclosure; Page 28-30; 33pp; English.

The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell

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or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their pluripotential; phenotype after expansion, in vitro. The expanded cell
in an in vitro culture medium for a period sufficient for the progenitor
 populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoietic function to autologous or allogement recipients. The present sequence is mouse beta-catenin protein, Beta-catenin is a privotal player in the signalling pathway initiated by Wnt proteins, which are mediators of several developmental
 Sequence 781 AA;
 processes.
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Gaps ö Length 781; Indels Match 100.0%; Score 227; DB 22; Local Similarity 100.0%; Pred. No. 9.6e-25; es: 44; Conservative 0; Mismatches 0; Matches : 44; Conservative Query Match Best

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AAY33237 standard; peptide; 44

AAY33237;

(first entry) 18-NOV-1999

Human, beta-catenin protein mutant armadillo repeat arm 8.

Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1; modulator; interaction domain; transcription factor; TCF-4; oncogenic; tumor suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; Wnt signalling, pathway; tumor development; anti-oncogenic; metanoma; organ regeneration; tissue regeneration; hair growth; mutant. 

sapiens сшон

Synthetic.

DE19909251-A1.

26-AUG-1999.

99DE-1009251 22-FEB-1999; 98DE-1007390 21-FEB-1998; (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

Von Kries J; Birchmeier W,

WPI; 1999-470389/40.

Agents for treating human diseases, particularly cancer, modula interaction of beta-catenin with transcription factors or tumor Agents for treating human diseases, suppressor gene products

Example 4; Fig 5; 16pp; German.

This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptides and related molecules (III) from the armadillo domain (arm units 3-8) of beta-catenin, and mutants of the compliste beta-catenin molecule, that include at least one of the

Length 840;

at ftp.wipo.int/pub/published\_pct\_sequences

840 AA;

Sequence

SXC

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0;
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences senomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
 E-cadherin; and (c) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin is a key compound in the Wht signalling pathway and is involved in development of tumors. Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic. (A) which inhibit interaction are particularly used to treat tumors, especially carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth. AAV33230-Y33241 represent mutant human beta-catenin armadillo repeat fragments described in the method of
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 Gaps
 developmental biology; cell signalling; insecticide;
 ;
0
 conductin
 Disclosure; SEQ ID NO 7380; 21pp + Sequence Listing; English.
 Length 44;
 Indels
 44
 specific interaction domains for LEF-1, TCF-4, APC,
 Drosophila melanogaster polypeptide SEQ ID NO 7380.
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Score 225; DB 20;
Pred. No. 6.7e-26;
 1; Mismatches
 EW.
 Myers
 Ą
 ABB60196 standard; Protein; 840
 PWD,
 99.1%;
97.7%;
 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
 23-MAR-2001; 2001WO-US09231
 26-MAR-2002 (first entry)
 Query Match
Best Local Similarity 97.75
 Ľ
 Drosophila melanogaster
 Adams M,
 WPI; 2001-656860/75.
N-PSDB; ABL04299.
 (PEKE) PE CORP NY
 44 AA;
 WO200171042-A2.
 pharmaceutical
 the invention
 Drosophila;
 27-SEP-2001
 Venter JC,
 Seguence
 ABB60196;
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 ABB60196
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 13
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
 Gaps
 Gaps
 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB67737-ABB72072).
 Drosophila; developmental biology; cell signalling; insecticide;
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0
 Disclosure; SEQ ID NO 24249; 21pp + Sequence Listing; English.
 Length 840;
 Indels
 Indels
 435 nngrnkatvcqvggvdalvrtiinagdreeitepavcalrhlts 478
 44
 44
 Drosophila melanogaster polypeptide SEQ ID NO 24249.
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Score 187; DB 22;
Pred. No. 8.6e-19;
 Score 187; DB 22;
Pred. No. 8.6e-19;
 Pred. No. 8.667; Mismatches
 7; Mismatches
 Myers EW;
 ¥
 ABB65819 standard; Protein; 840
 Li PWD,
 82.48;
 82.4%;
75.0%;
 2000US-191637P.
2000US-0614150.
 23-MAR-2001; 2001WO-US09231
 (first entry)
 New isolated nucleic acid
genes from Drosophila and
Query Match
Best Local Similarity 75.0
Matches (33; Conservative
 Conservative
 Drosophila melanogaster.
 Venter JC, Adams M,
 2001-656860/75
 (PEKE') PE CORP NY
 Query Match
Best Local Similarity
Matches 13; Conserv
 840 AA;
 N-PSDB; ABL09922
 WO200171042-A2.
 interactions -
 pharmaceutical
 23-MAR-2000;
11-JUL-2000;
 26"MAR-2002
 27-SEP-2001.
 ABB65819;
 Sequence
 .
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 435
 WPI:
 ABB65819.
 RESULT
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Himan; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vinetary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibecterial; regene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
 AAPISS66 to AAFI6505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer
 Cellular receptor 2; CR2; binding site; BS; auto-immune disease; Epstein-Barr Virus; EBV; B lymphocyte; ligand.
 31 NUYKNKMMVCQVGGIEALVRIVLRAGDREDITEPAICALRHLTS 44
 21 nnsknktlytqnsgvealihailragdkdditepavcalrhlts
 73.1%; Score 166; DB 21;
68.2%; Pred. No. 3.9e-16;
vative 7; Mismatches 7;
 Claim 11; Page 1813-1815; 2338pp; English
 Ā
 AAR11354 standard; Protein; 700
 (HUMAY) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
 08 MAR-2000; 2000WO-US05988
 12-MAR-1999; 99US-0124270.
 Cellular Receptor 2 ligand
 (first entry)
 Best Local Similarity' 68.2
Matches 30; Conservative
 Rosen CA, Ruben SM;
 WPÏ; 2000-587513/55.
 345 AA;
 N-PSDB; AAF16013.
 Homo saplens.
 WO200055174-A1
 21"SEP-2000.
 03-JUN-1991
 invention.
 Sequence
 Synthetic.
 AAR11354;
 Query Match
 12;
 RESULT
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 is
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
 Gaps
 Drosophila; developmental biology; cell signalling; insecticide;
 ö
 Disclosure; SEQ ID NO 24255; 21pp + Sequence Listing; English.
 Human prostate cancer antigen protein sequence SEQ ID NO:1388.
 82.4%; Score 187; DB 22; Length 840; llarity 75.0%; Pred. No. 8.6e-19; Conservative 7; Mismatches 4; Indels
 44
 Drosophila melanogaster polypeptide SEQ ID NO 24255
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Myers EW;
 ABB65821 standard; Protein; 840 AA.
 AA.
 AAB56810 standard; Protein; 345
 PWD,
 23-MAR-2000; 2000US-191637P.
 23-MAR-2001; 2001WO-US09231
 (first entry)
 (first entry)
 Ľ
 Drosophila melanogaster
 Adams M,
 WPI; 2001-656860/75
 ABB57737 - ABB72072)
 Query Match
Best Local Similarity
Matches 33; Conserv
 (PEKE) PE CORP NY
 840 AA;
 N-PSDB; ABL09924
 WO200171042-A2.
 pharmaceutical
 interactions
 26-MAR-2002
 27-SEP-2001
 13-MAR-2001
 Venter JC,
 ABB65821;
 Sequence
 AAB56810;
 RESULT 10
 ABB65821
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Gaps

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64

à g XEXEXEX

Length 345; Indels allergy;

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hybridoma cultures can be boosted.
The compsn. can be administered to inhibit infection in vitro or in
 The ligand pref. includes a fragment indicated in the features, or the total protein. The ligand pref. contains only a single BS and has an amino acid sequence <100 (pref. <20) residues in length. The ligand may also comprise a plurality of fragment 389.394. A therapeutic compsn. contg. the polypeptide is used to stimulate or inhibit B lymphocyte proliferation in patients with B cell lymphoma. B lymphocytes and myeloma's can be stimulated in patients with immunodeficiencies and immunoglobulin secretion by
 ç
 DNA segment encoding CR-2 ligand and CR2 binding site - used treat auto-immune disease, B-cell lymphoma and inhibit Epstein-Barr virus infection
 ...309
:e= "fragment most pref. included"
 /note= "fragment most pref. included"
 /note= "fragment pref. inlcuded"
189..394
 'note= "fragment pref. included"
Location/Qualifiers 300..312
 Disclosure; Fig 1; 129pp; English.
 90US-0512118
 90WO-US05027
 89US-0404679
 INST BIOLOGIC
 vivo by Epstein-Barr Virus
See also AAQ11140-42.
 385..400
 'note=
 WPI; 1991-101864/14.
 700 AA;
 N-PSDB; AA011140
 (CALB-) CALIF
 Key
Binding-site
 Binding-site
 Binding-site
 Binding-site
 04-SEP-1990;
 08-SEP-1989;
 Lernhardt W;
 WO9103251-A.
 20-APR-1990;
 21-MAR-1991
 Sequence
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0
 Gaps
 ő
 Length 700;
 Indels
 44
 1 NNYKNKMWVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Score 166; DB 12;
Pred. No. 8.9e-16;
7; Mismatches 7;
 73.1%;
 Conservative
Query Match
Best Local Similarity
Matches 30; Conserv
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ischemnia reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral Sclerosis; platelet disorder; thrombooytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection;
 Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 Novel human secretory protein, Seq ID No 663.
 AAU28306 standard; Protein; 800 AA.
 (first entry)
 18-DEC-2001
 AAU28306;
 AAU28306
RESULT
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Gaps

4 ;

52.4%; Score 119; DB 22; Length 800; 63.0%; Pred. No. 9.4e-09; ive 5; Mismatches 8; Indels

Ouery Match Best Local Similarity 63.0 Matches 29; Conservative

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The interior relates to novel isolated numan secreted polypeptioes (1) and polypuroleotides (II). (II) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohy's disease, inflammatory conditions such as arthritis, nephritis, Crohy's disease, is chaemia-reperfusion injury, shock, sepais, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and perity perpheral nervous system diseases and neuropathies, such as Alzheimer's, continuous site of selections in addition, (I) is involved in chemotactic or chemokinetic activity, requilation of haematopolesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, inclsions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders or profections or regeneration and treatment of lung or liver fibrosis, reperfusion in respectation and expense e.g. multiple sclerosis, reperfusion injury in various tissues, various immune disorders e.g. fungal infections, autoimmuned disorders e.g. multiple sclerosis, remematoid arthritis, diabetes mellitus, myasthenia gravis, altergic fungal infections, autoimmuned manapolism, storage or elimination of altersy fat, lipid, protein, anabolism, carabolydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like number of immune responses. Advolz8995 represent novel human secreted protein amino activ
 The invention relates to novel isolated human secreted polypeptides (I)
 ď,
severe combined immunodeficiency; SCID; autoimmune disorder; allergy multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 Zhou
 Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
 Ren F, Ma Y, Zhou
R, Xue AJ, Wang J;
 Xu C, Wehrman T, Rei
7, Zhang J, Chen R,
 Example 2; SEQ ID No 663; 107pp; English.
 amino acid sequences of the invention.
 fertility; analgesic; pain; antigen.
 Drmanac RT,
 05-MAR-2001; 2001WO-US04942
 2000US-0616847,
2000US-0665363,
 2000US-0519705
 2000US-0574454
2000US-0596193
 Asundi V,
 2000US-0693267
 WPI; 2001-589934/66.
N-PSDB; AAS45206.
 Liu C, A
Yang Y,
 (HYSE-) HYSEQ INC.
 W0200166689-A2.
 Homo sapiens.
 13-SEP-2001.
 14-JUL-2000;
 20-OCT-2000;
 19-MAY-2000;
 07-MAR-2000;
 Tang YT,
Zhao QA,
 Sequence
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42
1 NNYKNKMMVC-QVGGIEALVRT--VLRAGDR-EDITEPAICALRHL
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AAB36462 standard; Protein; 797 AAB36462;

(first entry) 01-MAR-2001 Human plakophilin-3 protein SEQ ID NO:2

Plakophilin-3; PKP3; catenin-like protein; characterisation; diagnosis; desmosome; epithelial cell; skin disease; dermatological; gene therapy; vaccine.

Homo sapiens.

WO200066619-A2

09-NOV-2000

28-APR-2000; 2000WO-EP04389.

99EP-0870093 30-APR-1999; (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

Bonne Van Roy F,

WPI; 2000-687529/67. N-PSDB; AAC64792.

Nucleic acids encoding Plakophilin-3 polypeptides, useful for treating skin diseases and disorders of epithelial tissue associated with inappropriate Plakophilin-3 expression and activity -

Example 1; Fig 2; 132pp; English.

The present invention describes an isolated or recombinant nucleic acid molecule (I) encoding a Plakophilin-3 (PRF9), from humans, mice and Xenopus laevis. (I) has dermatological activity, and can be used in can be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRP9 expression, such as skin diseases and disorders affecting epithelial tissue. For example, (I) (and vectors containing first decreased PRP3 polypeptide may be used to treat disorders associated with decreased PRP3 expression by rectifying mutations or deletions in a patient's genome that affect the activity of PRP3 by expression a patient's genome that affect the activity of PRP3 by expressing inactive proteins or to supplement the patients own production of PRP3 polypeptides. Additionally, (I) may be used to produce PRP3, according to standard recombinant DNA methodology, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence which patients may be in need of restorative therapy. The PRP3 putypeptides may be in need of restorative therapy. The PRP3 putypeptides may be used as antigens in the anti-PRP3 antibodies and PRP3 antagonists may also be used as diagnostic and matagonists of PRP3 antagonists may also be used as diagnostic and matagonists of PRP3 antagonists may also be used as diagnostic and matagonists of perturb prevent assays (ELISA)). PRP3 is a catenin-like protein, which is present in desmosomes and wone and when the present sequence represents human are actived by the present sequence represents human and pages and pages and prevent sequence represents human and pages and pag PKP3, as given in the present invention.

797 AA; Sequence

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 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
 Gaps
 2
 Length 797;
 Indels
 43
 4 KNKMMVCQVGGIEALVRTV---LRAGDRED-ITEPAICALRHLT
 Score 58.5; DB 21;
Pred. No. 8.3;
 8; Mismatches
 AAM 19226 standard; Protein; 797 AA
 Human protein SEO ID, NO 1888.
Query Match 55.8%;
Best Local Similarity, 40.9%;
Matches 18; Conservative E
 2000US-0598075
 2000US-0620325
 2000US-0693325
2000US-0728422
 05-FEB-2001; 2001WO-US04098
 20000S-0654936
 2000US-0663561
 06-NOV-2001 (first entry)
 (HYSE:) HYSEQ INC
 WO200157190-A2.
 20 JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
 Hono sapiens
 03-FEB-2000;
 27: APR-2000;
 09-AUG-2001.
 AAM79226;
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u P, Xu C, Cao Y Chen R, Wang ZW; Tang YT, Liu C, Drmanac RT, Asundi V, Zhou Zhao QA, Wang D, Wang J, Zhang J, Ren F, Xue AJ, Yang Y, Wejhrman T, Goodrich R; WPI; 2001-476283/51. N-PSDB; AAK52359

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gΩ

Cao Y,

Zhon

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy

Claim 20; Page 4278-4280; 6221pp; English.

encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell-proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nammatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Measurements for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication. The invention relates to polynucleotides (AAK51456-AAK53435) and the

797 AA; Seguence

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|--------------------------------------------|---------------|
|                                            | Gaps          |
| 797;                                       | 5;            |
| Length                                     | Indels        |
| 22;                                        | 13;           |
| core 58.5; DB<br>red. No. 8.3;             | 8; Mismatches |
|                                            | ative         |
| milarity                                   | Conserva      |
| ch<br>1 Si                                 | 18;           |
| Query Match<br>Best Local Similarity 40.9% | Matches       |
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Search completed: July 29, 2002, 16:07:57 Job time: 647 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 16:05:10 ; Search time 57.6 Seconds (without alignments) 18.658 Million cell updates/sec Run on:

US-09-641-104A-11

Title: Perfect score:

227 1 NNYKNKMMYCQVGGIEALVR.....AGDREDITEPAICALRHLTS Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

231628 seqs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|            | Description              | Sequence 11. App. |                  |                   |      | Patent No. 5183745 | Sequence 4, Appli |                 | Patent No. 5183745 | Sequence 8, Appli | 7                | 6    | Sequence 8. Appli | Patent No. 5489533 | 10,       |                   |                 | 'n              | Sequence 8, Appli | 8               | 52   | ٦    | H                | ٦                 | 15                | equence 1,       | 9               | Sequence 6, Appli |
|------------|--------------------------|-------------------|------------------|-------------------|------|--------------------|-------------------|-----------------|--------------------|-------------------|------------------|------|-------------------|--------------------|-----------|-------------------|-----------------|-----------------|-------------------|-----------------|------|------|------------------|-------------------|-------------------|------------------|-----------------|-------------------|
| SOMETHINES | ΙD                       | US-08-982-785A-11 | US-08-982-785A-9 | US-08-982-785A-10 |      |                    | 785-4             | US-08-669-785-2 | 5183745-6          | US-08-982-785A-8  | US-08-982-785A-2 |      | -488-8            |                    | 19-697-10 | US-08-727-616A-10 | US-08-256-136-2 | US-08-950-737-2 | US-08-973-461A-8  | US-08-648-010-8 |      | -    | US-08-318-039A-1 | US-08-318-038D-15 | US-08-227-496C-19 | US-08-435-568A-1 | US-09-240-915-6 | US-09-591-435-6   |
|            | DB                       | 4                 | 4                | 4                 | 9    | 9                  | 4                 | 4               | 9                  | 4                 | 4                | 9    | 7                 |                    | 7         | 4                 |                 | 7               |                   |                 | -    |      | ٣                | т                 | 4                 | 4                | 4               | 4                 |
|            | Query<br>Match Length DB | 999               | 682              | 620               | 525  | 1489               | 1705              | 1706            | 1794               | 989               | 756              | 79   | 131               | 185                | 262       | 262               | 449             | 449             | 449               | 449             | 453  | 480  | 202              | 502               | 505               | 505              | 502             | 505               |
| ф          | Query<br>Match           | 24.7              | 23.1             | 22.7              | 22.5 | 22.5               | 22.5              | 22.5            | 22.5               | 22.2              | 22.2             | 21.6 | 21.6              | 21.6               | 21.6      | 21.6              | 21.6            | 21.6            | 21.6              | 21.6            | 21.6 | 21.6 | 21.6             | 21.6              | 21.6              | 21.6             | 21.6            | 21.6              |
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|            | Result<br>No.            | н                 | 7                | m                 | 4    | 2                  | 9                 | 7               | 8                  | 6                 | 10               | 11   | 12                | 13                 | 14        | 15                | 16              | 17              | 18                | 19              | 20   | 21   | 22               | 23                | 24                | 25               | 26              | 27                |

|     | Sequence 14, Appl | Sequence 14, Appl | Sequence 3, Appli | Sequence 3, Appli | Sequence 3, Appli | 1, 1            | Sequence 3, Appli | Sequence 118, App | Sequence 12, Appl | 3,              | Sequence 3, Appli | 87                | Patent No. 5284931 | Sequence 15, Appl | Sequence 17, Appl | 7, A            | 'n               | 2, 1            |
|-----|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|--------------------|-------------------|-------------------|-----------------|------------------|-----------------|
|     | US-08-464-083-14  | US-08-469-587A-14 | US-08-789-078-3   | US-08-752-633-3   | PCT-US95-04886-3  | US-07-618-286-1 | US-08-196-003-3   | US-08-483-389-118 | US-08-689-870-12  | US-08-933-824-3 | US-09-264-466-3   | US-09-009-490A-87 | 5284931-2          | US-08-227-496C-15 | PCT-US93-00031-17 | US-08-973-068-7 | US-08-982-785A-3 | US-08-881-706-2 |
|     | Н                 | 7                 | ~                 | ~                 | 'n                | Н               | -                 | 7                 | ~                 | m               | 4                 | 4                 | 9                  | 4                 | Ŋ                 | ო               | 4                | 4               |
|     | . 507             |                   | :                 | •                 |                   | :               |                   |                   |                   | ·               |                   |                   | •                  | .;                |                   | 161             | 44               | 1196            |
|     | 21.6              | 21:6              | 21.6              | 21.6              | 21.6              | 21:6            | 21.6              | 21.6              | 21;6              | 21.6            | 21:6              | 21:6              | 21.6               | 21.6              | 21.6              | 21.1            | 20.7             | 20.7            |
| ۔   | 49                | 49                | . 49              | 49                | 49                | ۰.<br>46        | 49                | 49                | 49                | 49              | 49                | 49                | 67                 | 49                | . 49              | 48              | : 47             | 47              |
| 1.5 | 28.               | 29                | 30 %              | 31                | 32 - 3            | 33              | 34                | 35 🗽              | 36                | 37              | 38.               | 39                | 401 121            | 41.14             | 4.2               | 43              | 44: ;;           | 4.5             |

## ALIGNMENTS

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Sequence.11, Application US/08982785A
Sequence.11, Application US/08982785A
Sequence.11, Application US/08982785A
Sequence.11, Application:
APPLICANT: Kosik, Kenneth S.
APPLICANT: ADOL, Jianhua
TITLE.OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: UUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES.
CORRESPONDENCE ADDRESS:
 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: ReatSEQ for Windows 95
SOFTWARE: ReatSEQ for Windows 95
SOFTWARE: ReatSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,785A
FILING DATE: US/02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
ATTORNEY AGENT: INFORMATION:
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 05311/018001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEEX: 200154
INFORMATION FOR SEC 1D NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 666-amino acids
TYPE: amino acids
 ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: WAS COUNTRY: USA ZIP: 02110-2804
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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us-09-641-104a-11.rai

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7
 Gaps
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 ij
 Length 620;
 **APPLICANT: DANCHIN, ANTOINE:GLASER, PHILLIPPE;KRIN, EVELYN; BARZU, OCTAVIEN;LADANT, DANIEL;ULLMAN, AGNES TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
 APPLICANT: DANCHIN, ANTOINE; GLASER, PHILLIPPE; KRIN, EVELYN;
 Length 525;
 BARZU, OCTAVIEN; LADANT; DANIEL; ULLMAN, AGNES
TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
BILOGGICAL USES
INUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
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 18;
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 DB 4;
 DB 6;
 OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
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 Score 51.5; D. Pred. No. 9.8;
 APPLICATION NUMBER: US/08/982,785A FILING DATE: 02-DEC-1997
PRIOR; APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
| FILING DATE: 02-DEC-1996
ATTORNEY_AGENT INFORMATION:
NAME: Freeman Union Number: 29,066
REGISTRATION NUMBER: 29,066
TELECOMMUNICATION INFORMATION:
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FILING DATE: 25-OCT-1989
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amino acid
 Query Match 22.7
Best Local Similarity 39.5
Matches 17; Conservative
 617/542-8906
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MEDIUM TYPE: Diskette
"COMPUTER: IBM COMPALI
 BIOLOGICAL USES
NUMBER OF SEQUENCES: 13
 ; MOLECULE TYPE: protein US-08-982-785A-10
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 02110-2804
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 5183745-2 :
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 TOPOLOGY:
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 5183745-4
 5183745-4
 QQ
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 23.1%; Score 52.5; DB 4; Length 682; 37.5%; Pred. No. 7.7; Live 8; Mismatches 16; Indels
 US-08-982-785A-10
Sequence 10, Application US/08982785A
Sequence 10, Application US/08982785A
GENERAL INFORMATION:
APPLICANT: Rosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
 APPLICANT: Kosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
WOMBER OF SEQUENCES: 13
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SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
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 5 NKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
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 05311/018001
 ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
 E: Fish & Richardson P.C.
225 Franklin Street
 Sequence 9, Application US/08982785A Patent No. 6258929
 NAME: Freeman, John W. REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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 GENERAL INFORMATION:
 RY: USA
02110-2804
 Boston
 STREET: 225 F
CITY: Boston
 ΜĀ
 ADDRESSEE:
 TOPOLOGY:
 CITY: BOS
STATE: MA
COUNTRY:
 US-08-982-785A-9
 CITY:
STATE:
 Query Match
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APPLICANT: Guiso, Nicole Tiffe of Adenyl TITLE OF INVENTION: Protective Epitopes Of Adenyl TITLE OF INVENTION: Cyclase-Haemolysin(AC-Hly), Their Application To TITLE,OF INVENTION: The Treatment Or To The Prevention Of Bordetella Infections
 Gaps
 Gaps
 4
 4
 ... riumegan, Henderson, Farabow, Garrett & Dunner 1300 I Street, N.W., Suite 700 Tashinaton
 APPLICANT: DANCHIN, ANTOINE; GLASER, PHILLIPPE; KRIN, EVELYN; BARZU, OCTAVIEN; LADANT, DANIEL; ULLMAN, AGNES; TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
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Best Local Similarity, 37.5%; Pred. No. 45;
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APPLICATION NUMBER: US/08/426,541
FILING DATE: 25-OCT-1989
 APPLICATION NUMBER: US/08/669,785 FILING DATE: 27-JUN-1996 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
 22.5%;
 TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
 GENERAL INFORMATION:
APPLICANT: Betsou, Fotini
APPLICANT: Sebo, Peter
APPLICANT: Guiso, Nicole
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Best Local Similarity 37.5
Matches 12; Conservative
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; NUMBER OF SEQUENCES: 13
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 NUMBER OF SEQUENCES: 4
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 Washington
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 TOPOLOGY: linear
 STRANDEDNESS:
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 ADDRESSEE:
STREET: 13
 COUNTRY:
 US-08-669-785-2
 CITY: W
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 5183745-6
 5183745-6
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 APPLICANT: Betsou, Fotini
APPLICANT: Sebo, Peter
APPLICANT: Guiso, Nicole
TITLE OF INVENTION: Protective Epitopes Of Adenyl
TITLE OF INVENTION: Cyclase-Haemolysin(AC-Hly), Their Application To
TITLE OF INVENTION: The Treatment Or To The Prevention Of Bordetella Infections.
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 CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
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 Length 1705;
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Pred. No. 36;
 DB 4;
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Pred. No.
APPLICATION NUMBER: US/08/426,541
FILING DATE: 25-OCT-1989
 Sequence 4, Application US/08669785
Patent No. 6309648
 US-08-669-785-2
; Sequence 2, Application US/08669785
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25.146
REFERENCE/DOCKET NUMBER: 02:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
 22.5%;
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5183745-2
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 Matches
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Gaps
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 Length 756;
 Patent No. 5284931

Patent No. 5284931

STEVEN D. JOSTIN, MICHABL L.

TITLE OF INVENTION: INTERCELLULAR ADHESION MOLECULES AND THEIR BINDING LIGANDS

NUMBER OF SEQUENCES: 41

CURRENT APPLICATION DATE: US/07/515,478

FILING DATE: 27-APR-1990
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APPLICATION NUMBER: US/08/982,785A
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
-APPLICATION NUMBER: US 60/031,556
FILING DATE: 02-DEC-1996
ATTORNEY AGENT: INFORMATION:
NAME: Freeman, John W.
REGISTRATION WUMBER: 29,066
REGISTRATION WUMBER: 29,066
REGISTRATION WUMBER: 29,066
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REFERENCE/DOCKET NUMBER: 05311/018001
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 Jacobs, Kenneth
McCoy, John
LaVallie, Edward
Racie, Lisa
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 IBM Compatible
 Query, Match 22.2
Best Local Similarity 39.5
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APPLICANT:
APPLICANT:
 TOPOLOGY:
 US-08-982-785A-2
 SEQ ID NO:7
 5284931.7
 qq
 Ω
 ij
 Gaps
 1;
 APPLICANT: Kosik, Kenneth S.
APPLICANT: Zhou, Jianhua
TITLE OF INVENTION: ALARM RELATED PEPTIDES AND
TITLE OF INVENTION: NUCLEIC ACIDS AND DIAGNOSIS USING THEM
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
 APPLICANT: Kosik, Kenneth S. APPLICANT: Zhou, Jianhua TITLE OF INVENTION: ALARM RELATED PEPTIDES AND TITLE OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: Franklin Street CITY: Boston
 Length 686;
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 188 NDDNKIALKNCGGIPALVRLLRRTTDLE-IRELVTGVLWNLSS 229
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Pred. No. 16;
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OPERATING SYSTEM: Windows 95
OPTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,785A
FILING DATE: 0.2-DEC-1997
PRIOR APPLICATION DATA:
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 29,066
ER: 05311/018001
 APPLICATION NUMBER: US 60/031,556 FILING DATE: 02-DEC-1996 ATTORNEY/AGENT INFORMATION:
 ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
 Sequence 8, Application US/08982785A Patent No. 6258929 GENERAL INFORMATION:
 Sequence 2, Application US/08982785A Patent No. 6258929 GENERAL INFORMATION:
 NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0531
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
 22.2%;
39.5%;
 TELEVAL. 200154

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Matches 17; Conservative
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 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-982-785A-8
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MEDIUM TYPE: Diskett
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 USA
 STATE: MA
COUNTRY:
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 US-08-982-785A-2
 STATE: M
 Query Match
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us-09-641-104a-11.rai

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AND RAPID, FUNCTIONAL IDENTIFICATION OF GENOMIC POLYNUCLEOTIDES AND SECONDARY SCREENING CAPABILITIES
 Gaps
 5
 ;
 APPLICANT: Whitney, Michael A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SENSITIVE
TITLE OF INVENTION: METHOD RAPID, FUNCTIONAL IDENTIFICATION OF
TITLE OF INVENTION: POLYNUCLEOTIDES AND SECONDARY SCREENING
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 DB 6; Length 185;
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APPLICATION NUMBER: US/08/719,697
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 ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
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 08366/003001
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Best Local Similarity 29.4%; Pred. No. 4
Matches 10; Conservative 11; Mismatch
 ; Sequence 10, Application US/08727616A
 Sequence:10, Application US/08719697
Patent No. 5928888
GENERAL, INFORMATION:
 NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08:
TELECOMMUNICATION:
TELEPHONE: 619/678-5070
 26-SEP-1996
N: 435
 FILING DATE: 26-SEP-1996
GLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
FILING DATE: ,03-MAY-1988
 APPLICATION NUMBER: 250, FILING DATE: 28-SEP-1988
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 RESULT 14
US-08-719-697-10
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 ò
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 APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Bownan, Michael
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
 Length 131;
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/721,488
 Score 49; DB 2;
Pred. No. 3.3;
 7; Mismatches
 2 NYKNKMMVCQVGGIEALVRTVLRAGDREDITEP 34
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,814
FILING DATE: 06-FEB-1995
FRILNG DATE: 06-FEB-1995
APPLICATION NUMBER: 89,3075
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: 89,307
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: 454,294
FILING DATE: 2-DEC-1989
APPLICATION NUMBER: 45,963
FILING DATE: 04-MAY-1987
APPLICATION NUMBER: 115,798
FILING DATE: 02-NOV-1987
APPLICATION NUMBER: 115,798
FILING DATE: 16-FEB-1988
FILING DATE: 16-FEB-1988
APPLICATION NUMBER: 115,798
FILING DATE: 16-FEB-1988
 3: Genetics Institute, Inc.
87 CambridgePark Drive
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 8:
 Ouery Match 21.6%;
Best Local Similarity 36.4%;
Matches 12; Conservative
Merberg, David
 : 131 amino acids
amino acid
 SEQUENCE CHARACTERISTICS
 STREET: 87 Cambridge CITY: Cambridge STATE: Massachusetts
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-721-488-8
 424
 COUNTRY: U.S.A. ZIP: 02140
 CLASSIFICATION:
 STRANDEDNESS:
 ; Patent No. 5489533
 FILING DATE:
 ADDRESSEE:
 ICAM-2
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us-09-641-104a-11.ral
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Tue Jul 30 08:15:26 2002

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APPLICANT: Tsien, Roger Y.
APPLICANT: Zlokarnik, Gregor
TITLE OF INVENTION: SUBSTRATES FOR BETA-LACTAMASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolia
STATE: CA
COUNTRY: GA
ZIP: 92037
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EASTERD Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,616A
FILING DATE: 15-CCT-1996
PRIOR APPLICATION NUMBER: 38,347
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET
 ; MOLECULE TYPE: protein
; FRACMENT TYPE: internal
US-08-727-616A-10
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:| :: |:| |:| :: | | ::| | 100 DNAAQNLILKQIGGPESLKKELRKIGD--EVTNP 131

1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEP 34

δ

Gaps

Query Match 21.6%; Score 49; DB 4; Length 262; Best Local Similarity 29.4%; Pred. No. 8.1; Matches 10; Conservative 11; Mismatches 11; Indels

Search completed: July 29, 2002, 16:05:12 Job time: 482 sec

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version 4.5 - 2000 Compugen Ltd.
GenCore
Copyright (c) 1993
```

OM protein - protein search, using sw model

July 29, 2002, 16:09:16; Search time 70.63 Seconds Run on:

(without alignments)
59.860 Million cell updates/sec

US-09-641-104A-11
227
1 NNYKNKMWVCQVGGIEALVR.....AGDREDITEPAICALRHLTS Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

. 283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description              | beta-catenin - Afr | beta-catenin - hum | 4      | hypothetical prote | armadillo segment | beta-catenin - Hyd | hypothetical prote | plakoglobin - mous | plakoglobin, desmo | . '    | beta-catenin - Cae | armadillo protein | VAC8 protein - yea | hypothetical prote | hypothetical prote | aminotransferases | aminotransferases | probable iron-cont | hypothetical prote | H+-transporting AT | H+-transporting AT | probable ATPase - | chemotaxis respons | conserved hypothet | hypothetical prote | hypothetical prote | gene p120 protein | hypothetical prote | hypothetical prote |
|-----------|--------------------------|--------------------|--------------------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| SUMMARIES | ID                       | 835099             | A38973             | S35091 | S33793             | T12689            | JC4835             | 533794             | 835092             | A32905             | S35093 | T23341             | T43175            | S50446             | T48431             | T07721             | AF1200            | AD1558            | A83503             | н90029             | A45598             | S72845             | F70512            | B72346             | T37934             | T47638             | T29445             | S28498            | T26395             | A72711             |
|           | DB                       | 7                  | 7                  | 7      | 7                  | 7                 | N                  | 7                  | 7                  | 7                  | 7      | 7                  | 7                 | 7                  | 7                  | 7                  | 7                 | 7                 | 7                  | 7                  | Н                  | 7                  | 7                 | 7                  | 7                  | 7                  | ~                  | 7                 | 7                  | 7                  |
|           | Query<br>Match Length DB | 781                | 781                | 781    | 817                | 843               | 806                | 820                | 621                | 744                | 738    | 678                | 811               | 578                | 825                | 509                | 381               | 381               | 393                | 984                | 1011               | 609                | 609               | 120                | 564                | 727                | 380                | 911               | 1050               | 291                |
| æ         | Query<br>Match           | 100.0              | 100.0              | 100.0  | 88.1               | 82.4              | 79.7               | 75.3               | 73.1               | 73.1               | 67.0   | 57.7               | 32.6              | 26.4               | 26.2               | 25.8               | 25.3              | 24.9              | 24.0               | 24.0               | 23.8               | 23.6               | 23.6              | 23.3               | 23.3               | 23.3               | 23.1               | 23.1              | 23.1               | 22.9               |
|           | Score                    | 227                | 227                | 227    | 200                | 187               | 181                | 171                | 166                | 166                | 152    | 131                | 74                | 09                 | 59.5               | 58.5               | 57.5              | 56.5              | 54.5               | 54.5               | 54                 | 53.5               | 53.5              | 53                 | 53                 | 53                 | 52.5               | 52.5              | 52.5               | 52                 |
|           | Result<br>No.            | -                  | 7                  | m      | 4                  | S                 | 9                  | 7                  | 8                  | 6                  | 10     | 11                 | 12                | 13                 | 14                 | 15                 | 16                | 17                | 18                 | 13                 | 20                 | 21                 | 22                | 23                 | 24                 | 25                 | 26                 | 27                | 28                 | 29                 |

|                                                                         | unknown protein F2 | transcription-repa | 367K tegument prot | arginine decarboxy | arginine decarboxy | hypothetical prote | arginine decarboxy | chemotaxis signal | hypothetical prote | conserved hypothet | hypothetical prote | probable translati | adenylate cyclase | cyclolysin - Borde | variant surface gl | neural plakophilin |        |
|-------------------------------------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------|
|                                                                         | E96734             | E83658             | WZBEB6             | T02234             | T08104             | A82750             | T15046             | D97173            | AE0444             | AH2931             | F98350             | C71322             | S51672            | OYBRC              | B45522             | T42209             |        |
|                                                                         | 9 3 . 628 2        | 9, 11181 2         | **                 |                    |                    |                    | •                  | 31                | 5 158 2            | `                  |                    | •                  |                   | 5 1706 1           | -                  | 2 1247 2           |        |
| ير موج<br>در موجو<br>در ماد در موجو<br>در ماد در موجو<br>در ماد در موجو | 52 22              | 52 22:             |                    |                    | 51.5               |                    | 51.5               | . 51              | 1,1 22.5           | . 51               | 51                 |                    |                   |                    | 50.5 22:           |                    | , ma** |
|                                                                         | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                | 385                | 39                 | 40                 | 41                 | 42                | 43                 | 44                 | 45                 |        |

# ALIGNMENTS

RESULT 11 S35099. The content of a first can clawed frog cachenin - African clawed frog cachenin - African clawed frog cypecies: Xenopus laevis (African clawed frog) Cypecies: Xenopus laevis (African clawed frog) Cypecies: 350099 Sw. Crea. 135099 Sw. Crea. Cr

Gaps ö Length 781; Indels Ouery Match
Best Local Similarity 100.0%; Pred. No. 8.9e-23;
Matches 44; Conservative 0; Mismatches 0;

ö

(1 NNYKNKMAVQQVGGIBALVRTVLRAGDREDITEPAICALRHLTS 44 οp

RESULT: 2.

A38973.

beta-catenin - human

C; Species: Homo sapiens (mān)

C; Date: 26; Jan-1996, #sequence\_revision 08-Feb-1996 #text\_change 08-Oct-1999

R; Huelskeh; J; Bitchmeder, W; Behrens, J;

A; Reference number: A38973; MUID:95105247

A; Molecule type: mRNA

A; Residues: 1-781 KHCb>

A; Cross-references: GB:219054; NID:938519; PIDN:CAA79497.1; PID:938520

A; Residues: 1-781 Library, June 1995

A; Reference number: S55356:
A; Recession: S55356

A; Residues: preliminary

A; Molecule type: mRNA

A; Residues: 1-781 KNUL>
A; Residues: 1-781 KNUL>
A; Residues: 1-781 KNUL>
A; Cross-references: EMBL:X87838; NID:91154853; PIDN:CAA61107.1; PID:9860988

C; Comment: The cytoplasmic protein beta-catenin normally binds to a region in the cyt

1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS

δ a

Query Match 100.0%; Score 227; DB 2; Best Local Similarity 100.0%; Pred. No. 8.9e-23; Matches 44; Conservative 0; Mismatches 0;

```
C;Species: Hydra magnipapillata
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000
R;Accession: JC4835
R;Hobmayer. E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T.
Gene 172, 155-159, 1996
A;Title::Identification of a Hydra homologue of the beta-catenin/plakoglobin/armadill
A;Reference number: JC4835; MUID:96257271
 A;Title: Molecular analysis of the Armadillo locus: uniformly distributed transcripts A;Reference number: A31861; MUID:89211895
 A;Cross-references: GB:U36781; NID:g1407600; PIDN:AAC47137.1; PID:g1407601
C;Comment: This protein plays roles in cadherin-mediated cell adhesion and in signal
 ö
 ö
 A; Molecule type: DNA
A; Residues: 1-843 <FER>
A; Cross_treferences: EMBL: ALO21106; NID:e1371406; PID:e1249776; PIDN:CAA15946.1
A; Experimental source: clone cosmid 63B12
R; Riggleman, B.; Wieschaus, E.; Schedl, P.
Genes Dev. 3, 96-113, 1989
 armadilio segment polarity protein - fruit fly (Drosophila melanogaster)
N.Alternate names: protein 86E4.6
C.Species: Drosophila melanogaster
C.Date: 13-Aug-1999 * seguence_revision 13-Aug-1999 * text_change 21-Jul-2000
C.Accession: T12689; A31861
R.Ferraz; C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
Submitted to the EMBL Data Library, January 1998
A. Bescription: Sequencing the distal X chromosome of Drosophila melanogaster.
 Gaps
 Gaps
 A; Molecule type: DNA
A; Residues: 1-843 <RIG>
A; Crostates: EMBL:X54468; NID:97610; PIDN:CAA38350.1; PID:97611
C; Genetics:
 ö
 ;
0
 Length 806;
 Length 843;
 4; Indels
 Indels
 44
 . 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
 RESULT 7
S33794
hypothetical protein - sea urchin (Tripneustes gratilla)
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITËPAICALRHLTS
 Score 187; DB 2;
Pred. No. 2.8e-17;
7; Mismatches 4
 Score 181; DB 2;
Pred. No. 1.8e-16;
5; Mismatches 4
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A;Cross-references: FlyBase:FBgn0000117
A;Introns: 11/1; 557/3; 624/3; 715/3; 748/1
A;Note: 86E4.6
 A; Status: nucleic acid sequence not shown
 9
 beta-catenin - Hydra magnipapillata
 82.4%;
ilarity 75.0%;
Conservative
 Ouery Match 79.7%;
Best Local Similarity 77.3%;
Matches' 34; Conservative
 Keywords: cytoskeleton
 Best Local Similarity
Matches 33; Conserv
 A; Molecule type: mRNA
A; Residues: 1-806 <HOB>
 A; Accession: T12689
 A; Accession: A31861
 C;Genetics:
A;Gene: betaCtn
 Query Match
 Query Match
 .
9
 489
 RESULT
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 Apported to the converse of th
 Comment: Cellular levels of beta-catenin are regulated in part by the adenomatous polycancerous cell growth.
 ö
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 ö
 C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C; Accession: S35091
A; Tatle: Plakoglobin and beta-catenin: distinct but closely related.
A; Reference number: S35091, MuID:92376536
A; Status: prellminary
A; Residues: 1-781 kBUT>
A; Molecule type: mRNA
A; Residues: 1-781 kBUT>
A; Cross-references: EMBL:M90364; NID:g192141; PIDN:AAA37280.1; PID:g192142
C; Keywords: cytoskeleton
 Gaps
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 ;
0
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0
 ó
 781;
 781;
 Length 817;
microfilament network.
C;Comment: Cellular levels of beta-catenin are regulated in part cancerous cell growth.
C;Genetics:
A;Genetics:
A;G
 Indels
 Indels
 Indels
 Length
 Length
 430 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 473
 430 NNYKNKMMYCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 473
 44
 44
 44
```

1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS

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100.0%; Score 227; DB 2; 100.0%; Pred. No. 8.9e-23; iive 0; Mismatches 0;

Query Match
Best Local Similarity 100.0
Matches 44, Conservative

1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS

452

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δ

RESULT

Score 200; DB 2; 1 Pred. No. 4.5e-19; 5; Mismatches 2;

88.1%; ilarity 84.1%; Conservative

Local Similarity es 37; Conserv

Matches

Query Match Best Local 8

```
embryos of Xenopus laevis
 A, Experimental source: clone KOSC4.6
A, Experimental source: clone KOSC4.6
S.Costa, M.; Raich, W.; Agbunay, C.; Hardin, J.; Priess, J.R.
S.costa, M.; Raich, W.; Agbunay, C.; Hardin, J.; Priess, J.R.
A, Description: A putative catenin-cadherin system mediates morphogenesis of the C.
A, Reference number: Z22085
A, Rocession: T42221
 ö
 ö
 A; Accession: T23341
A; Status: preliminary; translated from GB/EWBL/DDBJ
A; Status: preliminary; translated from GB/EWBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-678 < WILL>
A; Cross-references: EMBL: 281564; PIDN: CAB04572.1; GSPDB: GN00019; CESP: K05C4.6
 C; Species: Xenopus laevis (African clawed frog)
C; Date: 06 Jan-1995 #sequence_revision 06 Jan-1995 #text_change 21-Jul-2000
C; Accession: 835093; S24636
R; Fouquet, B.; Zimbelmann, R.; Franke, W.W.
Differentiation 51, 187-194; 1992
A; Title: Identification 61, plakoglobin in oocytes and early embryos of Xenop A; Reference number: 835093; MUID:9309332
 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 A/Accession: S35093.
A/Status: preliminary
A/Roceule.type: mRNA
A/Roceule.type: mRNA
A/Roceule.type: mRNA
A/Roceule.type: mRNA
A/Roceule.type: mRNA
A/Roceule.type: mRNA
A/Roceule.type: mRNL
A/Roceule.type: mRNA
A/Roceul
 Gaps
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 Length 678;
 Length 738;
 Indels
 Indels
 420 NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLTS 463
 44
 44
 **1.NNYKNKMWVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 67.0%; Score 152; DB 2; I
59.1%; Pred. No. 1.5e-12;
iive 10; Mismatches 8;
 57.7%; Score 131; DB 2;
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Cross-references: EMBL: AF016853; PIDN: AAB94552.1
 C; Accession: T23341; T42221
R; Harris, B.
submitted to the EMBL Data Library, November 1996
A; Reference number: Z19729
 Mismatches
 beta-catenin - Caenorhabditis elegans
 A; Introns: 14/1; 235/1; 290/1; 620/3
 ′,
 plakoglobin - African clawed frog
 Best Local Similarity 59.18
Matches 26; Conservative
Conservative
 A; Molecule type: mRNA . A; Residues: 1-678 <COS>
 30;
 position:
 Query Match
 Query Match
 RESULT 110.
 Matches
 õ
 q
 ò
 R.Rosenthal, E.
Biochim. Blophys. Acta 1173, 337-341, 1993
A.Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver
A.Reference number: S33793; MUID:93305730
A.Accession: S37794
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-820 <ROS>
 C;Accession: A32005
R;Franke, W.W.; Goldschmidt, M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cowin, Proc. Natl. Acad. Sci. U.S.A. 86, 4027-4031, 1989
A;Title: Molecular cloning and amino acid sequence of human plakoglobin, the common jund A;Reference number: A32905; MUID:89264555
 ö
 ö
 Diakoglobin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S35092
R:Butz, S.; Stappert, J.; Weissig, H.; Kemler, R.
Science 257, 1142-1144, 1992
A;Fitle: Plakoglobin and beta-catenin: distinct but closely related.
A;Reference number: S35091; MUID:92376536
 plakoglobin, desmosomal - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 29-Aug-1997
 Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
 Gaps
 Gaps
 ö
 ;
0
 Length 744;
 Length 621;
 Length 820;
 3; Indels
 Indels
 297 NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLTS 340
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Score 166; DB 2; L
Pred. No. 1.5e-14;
7; Mismatches 7;
 75.3%; Score 171; DB 2;
68.2%; Pred. No. 4.1e-15;
Live 11; Mismatches 3.
 Score 166; DB 2;
Pred. No. 1.8e-14;
 A;Cross-references: GDB:126565; OMIM:173325
A;Map position: 7pter-7qter
C;Keywords: cytoskeleton
 73.1%;
68.2%;
 Query Match 73.1%;
Best Local Similarity 68.2%;
Matches 30; Conservative
 C; Species: Tripneustes gratilla
 30; Conservative
 Cross-references: GB:M23410
 Query Match
Best Local Similarity
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-744 <FRA>
 Best Local Similarity
 A; Gene: GDB:JUP
 Query Match
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hypothetical protein FBFG.250 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: P.O.Apr.2000; #sequence_revision 20-Apr.2000 #text_change 28-Jul-2000
C:Accession: T46431
R:Bevan, W.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stlekema, W.; Bancroft, Submitted to the Protein Sequence Database, March 2000
A:Reference number: 224488
A:Accession: T48431
A:Accession: preliminary
 Gaps
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 1;
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 A;Introns: 474/3; 522/3
A;Note: F8F6.250
C;Superfamily: Arabidopsis thallana hypothetical protein F8F6.250
 DB 2; Length 509;
 Indels
 Indels
 14; Indels
 115 NNENKLLIVEMGGLEPLINQMM--GDNVEVQCNAVGCITNLAT 155
 44
 A:Experimental source: cultivar Columbia; BAC clone F8F6 C;Genetics:
 298 ENKMVIGVLGAVEPILH-ALRSSESERARQDAALALYHLS 336
 15;
 11;
 2 NYKNKMMYCOVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 4 KNKMWYCQVGGTEALVRTVLRAGDREDITEPAICALRHLT 43
 DB 2;
 Query Match
25.8%; Score 58.5; Di
Best Local Similarity 35.0%; Pred. No. 5.8;
Matches 14; Conservative 10; Mismatches
 Score 59.5; Di
Pred. No. 6.9;
8; Mismatches
 298 OLGGVFSIVKRVMTQGALHDIRQ-LOCMLRNLTS 330
 ; Pred. No. 4.1;
16; Mismatches
 11 OVGGIEALVRIVLRAGDREDITEPAICALRHLTS 44
 completed: July 29, 2002, 16:09:17 Ne: 727 sec
 A, Molecule type: DNA
A, Residues 1-825 <BEV>
A, Cross references: EMBL:AL162873
 Cuery Match
Best Local Similarity 41.2%;
Matches, 14; Conservative
 25.6%;
 11; Conservative
Best Local Similarity
 A;Gene: ATSP:T23J7.150
A;Map position: 3
 A, Map position: 5
 Query Match
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 C; Genetics:
 Matches.
 RESULT, 15
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 RESULT #14
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 N'Alternate names: protein YEL013w
N'Alternate names: protein YEL013w
Cispeciaes: Saccharomyces cerevisiae
Cispeciaes: Sacharomyces cerevisiae
Cispeciaes: Sacharomyces cerevisiae
CiAccession: 550446
R:Dietrich, F.S.
R:Dietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A:Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 and A:Accession: 550428
A:Accession: 550428
A:Recience number: 550428
 A:Gene: bar-1; C54bl.6
A:Map position: X
A:Introns: 23/2; 65/3; 97/3; 132/3; 181/3; 223/2; 261/3; 332/3; 414/3; 452/3; 500/3; 542
 C;Function:
A;Description: required for vacuole inheritance and protein targeting from the cytoplasm
C;Keywords: yeast vacuole
 armadillo protein homolog BAR-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43175; T28813
R;Eisenmann, D.M.; Maloof, J.N.; Simske, J.S.; Kenyon, C.; Kim, S.K.
Submitted to the EMBL Data Library, May BAR-1 and LET-60 Ras coordinately regulate the hoscaription: The beta-catenin homolog BAR-1 and LET-60 Ras coordinately regulate the
 Cross-references: EMBL:U18530; NID:g602367; PID:g602380; GSPDB:GN00005; MIPS:YEL013w
 5;
 ö
 A; Description: The sequence of C. elegans cosmid C54D1.
A; Description: The sequence of C. elegans cosmid C54D1.
A; Reference number: 220527
A; Accession: T28B13
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-811 ANN>
A; Cross-references: EMBL:U46673; PIDN:AAC48154.1; GSPDB:GN00028; CESP:C54D1.6
A; Experimental source: strain Bristol N2; clone C54D1
 Gaps
 Gaps
 ;
0
 1 NNYKNKMMVCQVGGIEALVRTVLRA----GD-----REDITEPAICALRHL 42
 Length 811;
 Length 578;
 Score 74; DB 2; Length 811
Pred. No. 0.071;
3; Mismatches 18; Indels
 Indels
 44
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Pred. No. 9.8e-10;
8; Mismatches 12;
 DB 2;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
A;Residues: 1-811 <EIS>
A;Cross-references: EMBL:AF063646; PIDN:AAC17424.1
 A;Gene: SGD:VAC8; MIPS:YEL013w
A;Cross-references: SGD:S0000739; MIPS:YEL013w
A;Map position: 5L
C;Function:
 Score 60;
 32.6%;
 26.48;
 Local Similarity 54.5%;
nes 24; Conservative
 Query Match
Bost Local Similarity 38.3.
Thes 21; Conservative
 A; Reference number: Z22328
A; Accession: T43175
 Query Match
 Genetics:
 RESULT 13
S50446
 Best Loc
Matches
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 16:09:55; Search time 34.24 Seconds (without alignments) 49.756 Million cell updates/sec Run on:

Perfect score: Sequence:

US-09-641-104A-11
227
1 NNYKNKMWVCQVGGIEALVR.....AGDREDITEPAICALRHLTS

44

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to:have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

| Description           | p35222 homo sapien | mus m      | ratt     | xenopus    | urechis    | _         |           | P35223 tripneustes | _          | P14923 homo sapien | xenop      | P39968 saccharomyc | Q9y446 homo sapien |           |            |            | Q56312 thermotoga | P30999 mus musculu | O60716 homo sapien | _          | _          |            | 000192 homo sapien |            |            | Q57506 bordetella | P15318 bordetella | P25547 agrobacteri |            | Q24186 drosophila | 00000000000 + 77 L LOG | FO##// CT Ypanosoma |
|-----------------------|--------------------|------------|----------|------------|------------|-----------|-----------|--------------------|------------|--------------------|------------|--------------------|--------------------|-----------|------------|------------|-------------------|--------------------|--------------------|------------|------------|------------|--------------------|------------|------------|-------------------|-------------------|--------------------|------------|-------------------|------------------------|---------------------|
| SUMMARIES             | CTNB HIMAN         | CTNB_MOUSE | CTNB_RAT | CTNB_XENLA | CTNB_URECA | ARM_DROME | ARM_MUSDO | CTNB_TRIGR         | PLAK_MOUSE | PLAK_HUMAN         | PLAK_XENLA | VAC8_YEAST         | PKP3_HUMAN         | ATC_TRYBB | YL15_MYCLE | YL15_MYCTU | CHEY_THEMA        | CTD1_MOUSE         | CTD1_HUMAN         | PPNK_AERPE | TEGU_HSVEB | PKP3_MOUSE | ARVC_HUMAN         | EFG2_TREPA | PKP4_HUMAN | CYAA_BORBR        | CYAA_BORPE        | GBPR_AGRTU         | PFPA_SOLTU | $\Box$            | DOVOT LUNG             | 1                   |
| Length DB             | 781 1              | 781 1      |          |            |            |           |           |                    |            |                    |            |                    |                    |           |            | 609        | 120 1             | 911 1              | 968 1              | 291 1      | 3421 1     | 797 1      |                    |            |            |                   |                   |                    | 616 1      |                   |                        |                     |
| %<br>Query<br>Match L | 100.0              | 100:0      | 100.0    | 100.0      | œ          | 82.4      | 81.1      | 75.3               | 73.1       | 73.1               | 67.0       | 26.4               | 25.8               | 23.8      | 23.6       | 23.6       | 23.3              | 23.1               | 23.1               | 22.9       | 22.9       | 22.7       | 22.7               | 22.5       | 22.5       | 22.5              | 22.5              | 22.0               | 22.0       | 21.8              | α                      |                     |
| Score                 | 227                | 227        | 227      | 227        | 200        | 187       | 184       | 171                | 166        | 166                | 152        | 09                 | 58.5               | 54        | 53.5       | 53.5       | 53                | 52.5               | 52.5               | 52         | 52         | 51.5       | 51.5               | 51         | 51         | 51                | 51                | 20                 | ഹ          | 9                 |                        | ,                   |
| Result<br>No.         | 1                  | 7          | m        | 4          | S          | 9         | 7         | œ                  | თ          | 10                 | 11         | 12                 | 13                 | 14        | 15         | 16         | 17                | 18                 | 19                 | 20         | 21         | 22         | 23                 | 24         | 25         | 26                | 27                | 28                 | 29         | 30                |                        | 1 :                 |

|         |    | P05362 homo sapien | 058974 pyrococcus | Q9kbe4 bacillus ha | P29139 paenibacill | P18667 synechococc | Q96412 dianthus ca | P98203 mus musculu | Q9z6q0 chlamydia p | Q58588 methanococc | Q9zma9 helicobacte | 025097 helicobacte | Q00127 ictalurid h |    |                 |    |
|---------|----|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----|-----------------|----|
|         |    | ICA1_HUMAN         | YC09_PYRHO        | HUTI_BACHD         | ISP_PAEPO          | EFG_SYNP6          | SPE1_DIACA         | ARVC_MOUSE         | AMPM_CHLPN         | YB87_METJA         | ILVC_HELPJ         | ILVC_HELPY         | VG23_HSVI1         |    | ALIGNMENTS      |    |
|         |    | Н                  | H                 | ٦                  | -                  | Н                  | П                  | -                  | 7                  | -                  | 7                  | 7                  | ч                  |    |                 |    |
|         |    | 532                | 259               | 426                | .326               | 769                | 725                | 696 3.             |                    | 301                | 330                | 330                | 418                | •  |                 |    |
| . •     | -  | 21.6               | 21:4              | 21:4               | 21:1               | 21:1               | 21:1               | 20.9               | 20.7               | 20.7               | 20,7               | 207.               | 20:7               |    | ٠.              | ;  |
| <b></b> | 1. | 34 49              | 35 2 48.5         | 36 31 48.5         | 37. 1 48           | 38 48              | 39:1::, 48         | 401.147.5          | 41:15. 11 47       | 42 Kr 47           | 43.5 1.47          | 44,011 47          | 45 1 47            | 1. | L-70<br>-11 E f | 16 |

# ALIGNMENTS

|                    |          |       | STANDARD; PRT; 781 AA. | 28; Created)              | (Rel. 28, Last sequence update) | 41,:Last annotation update) |               | in plan )            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | ia;.Primates; Catarrhini; Hominidae; Homo. |                  |                         |               | MEDLINE=95105247; PubMed=7806582; | ns J.;       | NPC compete for the interaction with beta-catenin and | une cycoskereton;<br>J. Cell Biol, 127:2061-2069(1994). |     |         | MEDLINE=20145417; PubMed=10679188; | eta-catenin signaling in the Wnt pathway."; | Biochem Biophys. Res. Commun. 268:243-248(2000). |     | X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 133-664. | rer C:, Mao F:, Kimelman D:, Xu W:; | re of a beta-catenin/Tcf complex."; | cell 103:885-896(2000). | VOLVED IN THE REGULATION OF CELL ADHESION AND IN | -i-: SUBUNIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION | OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND | THE NUCLEAR FORM BINDS TCF/LEF-1 AND MAY ALSO BIND DIDLIN CAN HETERODIMERIZE WITH ALPHA-CATENIN AND | '- ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE | . OF THE CADHERIN COMPLEX TO THE CORTICAL ACTIN CYTOSKELETON. | SPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS | STABILIZED (LOW LEVEL OF PHOSPHORYLATION). | 7 PHOSPHORYLATED BY GSK-3B, WNI-DEPENDENT ACTIVATION<br>NITERS THE ACTION OF CSK-3B DHOSDHODYLATION OF BETA- | CATENIN IS REDUCED AND THE PROTEIN IS NO LONGER DEGRADED, | RESULTING IN ITS ACCUMULATION IN CYTOPLASM. | SELONGS TO THE BETA-CATENIN FAMILY. | CONTAINS 12 ARM REPEATS. | right. It is produced through | is Institute of Biointormatics and the EMBL outstation - | use burghean brothtormaries institutions as long as its content is in no way | s statement is not removed. Usage by and for commercial |
|--------------------|----------|-------|------------------------|---------------------------|---------------------------------|-----------------------------|---------------|----------------------|-------------------------------------------------------------------|--------------------------------------------|------------------|-------------------------|---------------|-----------------------------------|--------------|-------------------------------------------------------|---------------------------------------------------------|-----|---------|------------------------------------|---------------------------------------------|--------------------------------------------------|-----|---------------------------------------------------|-------------------------------------|-------------------------------------|-------------------------|--------------------------------------------------|-----------------------------------------------------------------------|--------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|---------------------------------------------------------------|-------------------------------------------------------|--------------------------------------------|--------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------|---------------------------------------------|-------------------------------------|--------------------------|-------------------------------|----------------------------------------------------------|------------------------------------------------------------------------------|---------------------------------------------------------|
|                    |          | :     | STANDA                 | (Rél. 28,                 | (Rel. 28,                       | (Rel41,                     | . divis       | (Human)              | etazoa; C                                                         | theria; F                                  | 506;             |                         | ta:           | 5247; Put                         | Birchmei     | and APC c                                             | 127:206                                                 |     |         | 5417; Pub                          | of beta-c                                   | ohys. Res                                        |     | LLOGRAPHY                                         | Weaver C                            | acture of                           | -896(2000               | : INVOLVE                                        | THE CYTC                                                              | EGRADÀTIC                                                          | IN THE N                                                                                            | A A TRIME                                                             | ADHERIN C                                                     | PHOSPHOF                                              | ED (LOW I                                  | SABLY PHO                                                                                                    | IS REDUCE                                                 | IN ITS                                      | IY: BELON                           | ry: CONTA                | ROT entry                     | Swiss In                                                 | profit                                                                       | this sta                                                |
| 1/m<br>4<br>5<br>7 | RESULT 1 | HUMAN | CTNB_HUMAN             | P35/2/2;<br>01 FEB-1994 ( | 01-FEB-1994 (                   | 01-MAR-2002                 | Beta-catenin. | Homo sapiens (Human) | Eukaryota; Me                                                     | Mammalia; Eut                              | NCBI_TaxID=9606; | [1]. CECITENCE EDON N A | TISSUE-Placer | MEDLINE=9510                      | Huelsken J., | "E-cadherin                                           | J. Cell Biol                                            | [2] | REVIEW. | MEDLINE=2014                       | "Requiation of                              | Biochem. Bior                                    | [3] | X-RAY CRYSTAI                                     | Gráham T.A.,                        | "Crystal stru                       | Cell 103:885            | - I - FUNCTION                                   | - i - SUBUNIT:                                                        | OF ITS DI                                                          | F-CADHER                                                                                            | - ALSO FOR                                                            | OF THE CA                                                     | LEVEL OF                                              | STABILIZA                                  | - I - PIM: PROI                                                                                              | CATENIN                                                   | RESULTING                                   | SIMILARI                            | SIMILARI                 | This SWISS-PI                 | between the Swiss Institute                              | use by non                                                                   | modified and                                            |
|                    | RESU     | CINB  | O S                    | A<br>P                    | DI                              | 티                           | D C           | S C                  | 88                                                                | 8                                          | <b>x</b> 0       | Z C                     | 1<br>2<br>2   | RX                                | RA           | RT                                                    | Z 12                                                    | RN  | RP      | Z d                                | R R                                         | R.                                               | RN  | RP<br>X                                           | RA<br>RA                            | RŢ                                  | RL                      | 35                                               | ខ                                                                     | ည                                                                  | 8                                                                                                   | 88                                                                    | ဗ္ဗ                                                           | 8                                                     | ဥ္ပ                                        | 8 5                                                                                                          | ខ                                                         | ႘                                           | ဥ                                   | 38                       |                               | ខ្ល                                                      | 8                                                                            | ပ္ပ                                                     |

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Pokutta S., Weis W.I.; "Structure of the dimerization and beta-catenin-binding region of
CTNNA1.
MEDLINE-20337986; PubMed-10882138;
 Repeat; 3D-structure
 781. AA;
 . 44;
 CTNB_RAT
Q9WU82;
 SEQUENCE
 SMA.RT;
 REPEAT
 3.
 REPEAT
 REPEAT
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 REFEAT
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 Matches
 CTNB_RAT
 RESULT
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
 Gaps
 Huber A.H., Nelson W.J., Weis W.I.; "Three-dimensional structure of the armadillo repeat region of beta-
 Mus musculus (Mouse).
Sukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
 PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 118-149 IN COMPLEX WITH
 ;
0
 MEDLINE-92376536; PubMed-1509266;
Butz. S., Stappert J., Weissig H., Kemler R.;
"Plakoglobin and beta-catenin: distinct but closely related.";
Science 257:1142-1144(1992).
 Length 781;
 "Regulation of beta-catenin signaling in the Wnt pathway."; Blochem. Biophys. Res. Commun. 268:243-248(2000).
 Indels
 CB78F165A3EEF86E CRC64;
 44
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 100.0%; Score 227; DB 1;
ilarity 100.0%; Pred. No. 1.9e-23;
Conservative 0; Mismatches 0;
 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 150-665
MEDLINE=97442350; PubMed=9298899;
 01-JUL-1993 (Rel. 26, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
 781 AA

 ARM 12
 MEDLINE=20145417; PubMed=10679188;
 InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
 ARM
ARM
ARM
ARM
ARM
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 ARM
 Created)
 MW;
 EMBL; X87838; CAA61107.1; -. EMBL; Z19054; CAA79497.1; -. PIR; S31988; S31988.
 85496
 STANDARD;
 Cell 90:871-882(1997).
 PDB; 1G3J; 17-JAN-01.
TRANSFAC; T02872; -.
 01-JUL-1993 (Rel. 26,
 ructure
 637
781 AA;
 Similarity
 SEQUENCE FROM N.A.
 CINNB1 OR CAINB.
 235
277
319
361
440
489
 Beta-catenin.
 MIM; 116806;
 44;
 CTNB_MOUSE
Q02248;
 Query Match
Best Local 8
 SEQUENCE
 Kikuchi
 REPEAT
REPEAT
REPEAT
REPEAT
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 RESULT 2
CINB_MOUSE
 REVIEW
 REPEAT
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 ö
Mol. Cell 5:533-543(2000).

Mol. Cell 5:533-543(2000).

SIGNAL TRANSDUCTION THROUGH THE WNT PATHWAY.

SIGNAL TRANSDUCTION THROUGH THE WNT PATHWAY.

-1-. SUBUNIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION

"OF ITS DEGRAPATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND

E-CADHERIN. THE NUCLEAR FORM BINDS TCF/LEF. AND MAY ALSO BIND

PONTINS: AND INTERIN CAN DEPREDADED TO THE CYTOSOLIC FORM ALSO BIND
 PONTINES AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATEMIN AND ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN. COMPLEX TO THE CORTICAL ACTIN CYTOSKELETON.

SUBCELLULAR LOCATION: CYTOPLASMIC WHEN IT IS UNSTABILIZED (HIGH LEVEL OF PHOSPHORYLATION). TRANSLOCATES TO THE NUCLEUS WHEN IT IS TABILIZED (LOW LEVEL OF PHOSPHORYLATION). PTM: PROBABLY PHOSPHORYLATION OF DYL ANTAGONIZES THE ACTION OF GSK-3B. PHOSPHORYLATION OF DYL ANTAGONIZES THE ACTION OF GSK-3B. PHOSPHORYLATION OF BETA-CATEMIN IS REDUCED AND THE PROTEIN IS NO LONGER DEGRADED,
 Gaps
 9.
Structural protein; Nuclear protein;
 ö
 Length 781;
 Indels
 M 11.
NM 12.
D708F170A3FBED6E CRC64;
 430 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 473
 44
 RESULTING IN ITS ACCUMULATION IN CYTOPLASM. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 12 ARM REPEATS.
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 ö
 Query Match 100.0%; Score 227; DB 1; Best Local Similarity 100.0%; Pred, No. 1.9e-23;
 A.
 0; Mismatches
 781
 ARM 3.
ARM 4.
ARM 5.
ARM 7.
ARM 9.
ARM 10.
ARM 11.
 12.64.0.7.00
 PTR, 235091; 335091.
PDB; 2BCT; 15-0CT-97.
PDB; 3BCT; 19-0V0-97.
PDB; 1DOW; 12-UL-00.
TRANSFAC; T02984; ---
MGD; MGIS B8276; Catnb.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
 ARM
ARM
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Cell adhesion; Cytoskeleton; 3
 85470 MW;
 EMBL; M90364; AAA37280.1; -.
 Conservative
 STANDARD;
 571
636
666
 SM00185; ARM; 11
 191
234
276
318
360
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1. SINYKNKMMVČOVGGIĒĀLVRTVLRAGDREDITEPAICALRHLTS 44 1. SINYKNKMMVČOVGGIĒĀLVRTVLRAGDREDITEPAICALRHLTS 44 1. SINYKNKMMVCQVGGIĒĀLVRTVLRAGDREDITEPAICALRHLTS 473

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 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 J. Ceil. Physiol. 181:258-272(1999).

-!- FUNCTION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN SIGNAL TRANSDUCTION THROUGH THE WIT PATHWAX (BY SINLLARITY).

-!- SUBUNIT: THE CYTOSOLIC FORM BOUND TO AKIN ALLOWS THE STIMULATION OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND E-CADHERIN. THE MUCLEAR FORM BINDS TCF/LEF-1 AND MAY ALSO BIND PONTINES AND DUPLIN. CAN HETERODIMBRIZE WITH ALPHA-CATENIN AND ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX TO THE CORTICAL ACTIN CYTOSKELETON (BY
 MEDLINE=99428593; PubMed=10497305; Chung S.S.W., Lee W.M., Cheng C.Y.; "Study on the formation of specialized inter-Sertoli cell junctions in
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 SUBCELLULAR LOCATION: CYTOPLASMIC WHEN IT IS UNSTABILIZED (HIGH
 Structural protein; Nuclear protein;
 M 12.
9C29186B6DD54B87 CRC64;
 (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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 HSSP; Q02248; ZBCT.
InterPro; IPR00Q225; Armadillo.
Pfam: PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
 ARM
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ARM
 ARM
 EMBL; AF121265; AAD28504.1; -.
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Cell adhesion; Cytoskeleton; S
 85454 MW;
 594
637
781 AA;
16-OCT-2001 (Rel.
 SEQUENCE FROM N.A.
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 1151
1193
2235
2277
319
361
442
442
 Beta-catenin.
 16-OCT-2001
01-MAR-2002
 REPEAT
SEQUENCE
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 ö
 -1- FUNCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL
ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
PROPERTIES. ESSENTIAL COMPONENT OF THE VERTEBRATE WNT-SIGNALING
PATHMAX AND IS REQUIRED FOR FORMATION OF THE BEBRYONIC AXIS.
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
 McCrea P.D., Turck C.W., Gumbiner B.M.; "A homolog of the armadillo protein in Drosophila (plakoglobin) associated with E-cadherin.";
 ;
0
 Length 781;
 Indels
 Structural protein; Repeat.
 3ECD27232239F799 CRC64;
 Score 227; DB 1;
Pred. No. 1.9e-23;
 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 781 AA
 0; Mismatches
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Brain;
 or send an email to license@isb-sib.ch).
 -!- SIMILARITY: CONTAINS 10 ARM REPEATS.
 Xenopus laevis (African clawed frog)
 MEDLINE=92073903; PubMed=1962194;
 ARM
ARM
ARM
ARM
ARM
ARM
 Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
BMRT; SM00185; ARM; IIP.
PROSITE; PS50176; ARM_REPPAT; 9.
Cell adhesion; Cytoskeleton; Stru
 ARM
 100.0%;
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 Science 254:1359-1361(1991)
 Matches , 44; Conservative
STANDARD;
 Xenopodinae; Xenopus.
 625
781 AA;
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Best Local Similarity
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 Beta-catenin.
 CTNB_XENLA
 SEQUENCE
 REPEAT
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 REPEAT
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44

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Gaps

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Length 781; Indels

100.0%; Score 227; DB 1; 100.0%; Pred. No. 1.9e-23;

Mismatches

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44; Conservative

Matches

Query Match Best Local Similarity

```
Drosophila melanogaster (Fruit fly).
Eŭkaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
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 ó
 Rosenthal E.T.;
"Identification of homologues to beta-catenin/plakoglobin/armadillo
in two invertebrates, Urechis caupo and Tripneustes gratilla.";
Blochim. Blophys. Acta 1173:337-341(1993).
-1- FUNCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL
ADHESION MOLECULE E-CADHERIN, AND PEHHAPS TO OFHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
 Gaps
 ó
 Urechis caupo (Innkeeper worm) (Spoonworm).
Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
NCBI_TaxID=6431;
 88.1%; Score 200; DB 1; Length 818; larity 84.1%; Pred. No. 1e-19; Conservative 5; Mismatches 2; Indels
 Structural protein; Repeat.
 1DF174BEEF745C1D CRC64;
430 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 473
 452 NNQRNKVTVCQVGGIEALVRTILQAGDREDITEPAVCALRHLTS 495
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
 -!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 AFM_DROME STANDARD; PRT; 843 AA. P18824; 002371; 09W456; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) AFM OR EG:86E4.6 OR CG11579.
 818 AA
 ARM 1.
ARM 2.
ARM 3.
ARM 4.
 ARM 6.
ARM 7.
 Pfam; PFO0514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
 MEDLINE-93305730; PubMed-8318544;
 InterPro; IPR000225; Armadillo
 89070 MW;
 EMBL; L10355; AAA30330.1; -. HSSP; 002248; 2BCT.
 Cytoskeleton;
 STANDARD;
 543
648
818 AA;
 Query Match
Best Local Similarity
Matches 37; Conserv
 [1]
SEQUENCE FROM N.A.
 Cell adhesion;
 Beta-catenin.
 CTNB_URECA
P35224;
 SEQUENCE
 REPEAT
REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 CTNB_URECA
 9
 ARM_DROME
 RESULT
g
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 a
 GEDTAC
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RAY MEDLINE—20196006; PubMed=10731132;

RA Admas M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amenatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Et. Li P.W., Hoskins R.A., Galle R.F.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Bradon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril, J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Basaley E.M.,

RA Ballew R.M., Basus M., Baxendale J., Bandari D., Bolanakov S.,

RA Ballew R.M., Basus D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Berson K.Y. Bencs P.V., Berman B.P., Bhandari D., Bolanakov S.,

RA Borkova D., Botchen M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Bordon K., Doup L.E., Downes M. Dugan Rocha S., Pleischman W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrac C., Ferrac C., Ferrac C., Gan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum R.A.,

RA Harris N.L., Harvey D., Hemman T.J., Hernandez J.R., Houck J.,

RA Adail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum R.A.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum R.A.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum R.A.,

Alali M., Kalush F., Karpen G.H., Ncleod M.P., McDherson D.,

Merkulvo G., Milshina N.V., Mobarry C., Morris J. Morphy D., Norleot J.,

Ra Bazzolo M., Dittand G.S., Pan S., Pollard J., Woller E., Shen H.,

Ra Bazzolo M., Dittand G.S., Pan S., Pollard J., Wang X.,

Ra Bazzolo M., Pittand G.S., Pan S., Pollard J., Wang S., Wang X.,

Ra Bazzolo M., Dittand S., Rangeron M., Skupski M.P., Saith T.,

Ra Spier E., Spradling A.C., Stapleton M., Strong K., Wang S., Wan R.,

Ra Mang Z.-Y., Woordage T., Worley K.C., Wu D., Yang S., Zhan M., Zhang S., Walland S., Wall
Ptěrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 SIRAIN_CARGOVER, F.
MEDÍLINE_20196011; PubMed=10731137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadleu E.,
Dreano S., Gloux S., Lelaure V., Mottler S., Gallbert F., Borkova D.,
Minana B., Kafatos F.C., Louls C., Siden-Kiamos I., Bolshakov S.,
 Riggleman B., Wieschaus E., Schedl P., "Molecular analysis of the armadillo locus: uniformly distributed transcripts and a protein with novel internal repeats are associated With a Drosophila segment polarity gene."; Genes'Dev. 3:96-113(1989).
 SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND ALTERNATIVE
 Loureiro J., Peifer M.;
"Rôles of Armadillo, a Drosophila catenin, during central nervous
system development.";
 SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
 SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
 SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
 MEDLINE-98298928; PubMed-9635189;
 MEDLINE-89211895; PubMed-2707602;
 Science 287:2185-2195(2000).
 Curr. Biol. 8:622-632(1998).
 STRAIN-OREGON-R;
 ST'RAIN-OREGON-R;
 STRAIN-BERKELEY
 Ephydroidea; Dr
NCBI_TaxID=7227
 TISSUE-Head;
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A MEDILIALIAN PRODUCED AS A MEDILIAL PROPERTY AND A MEDILIAL PROPERTY A MEDILIAL PROPERTY AND A MEDILIAL PRANSMISSION OF DEVELOPMENTAL INFORMATION. CAN ASSOCIATE WITH ALPHA-CATENIN. CYTOPLASMIC ISOFORM ACCUMULATES THROUGH WG SIGNALING. ARM FUNCTION IN WG SIGNAL TRANSMISSION OF DEVELOPMENTAL INFORMATION. CAN ASSOCIATE WITH ALPHA-CATENIN. CYTOPLASMIC ISOFORM ACCUMULATES THROUGH WG SIGNALING. ARM FUNCTION OF DETERMINATION OF NEUROBLAST FATE. ARM AND ABL PROTEINS FUNCTION COOPERATIVELY AT ADHERENS JUNCTIONS IN BOTH THE CNS AND PEDIBERMIS.

1- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED WITH THE COOPERATIVELY STOPLASMIC (SHOWN HERE) AND NEURAL; ARE PRODUCTS: 2 ISOFORMS; CYTOPLASMIC (SHOWN HERE) AND NEURAL; ARE PRODUCED BY ALTERNATIVE SPLICING.

1- TISSUE SPECIFICITY: CYTOPLASMIC ISOFORM IS PREDOMINANT BEFORE GERM DANN DEFINING AND PRIBLY AND DEFINING AND DEFINING AND PRIBLY AND DEFINING AND PRIBLY AND DEFINING
 BAND RETRACTION, AFTER RETRACTION AND DUBING LARVAL STAGES, IT IS FOUND IN HIGH LEVELS IN SPECIFIC CELLS ALONG THE CNS MIDLINE.

ROUND IN HIGH LEVELS IN SPECIFIC CELLS ALONG THE CNS MIDLINE.

ROUND IN HIGH LEVELS IN SPECIFIC CELLS ALONG THE CNS MIDLINE.

AXON TRACTS OF THE CNS, ALSO PRESENT IN AXONS DURING LARVAL STAGES AND ACCUMULATES IN THE MOTOR NEURONS OF THE SECHMENTAL AND INTERSEGEMENTAL AND INTERSEGEMENTAL AND ACCUMULATE IN THE POPS.

INTERSECEMENTAL NERVES AS THEY EXIT THE CNS. BOTH ISOFORMS ACCUMULATE IN THE POPS.

-!- DEVELOPMENTAL STAGE: PRESENT AT ALL STAGES, BUT REACHED THE HIGHEST LEVELS DURING EARLY TO MID-EMBRYOGENESIS.

-!- PIM: PROSPHORYLATED ON SER, THR AND TYR RESIDIDES. LEVEL OF PHOSPHORYLATION VARIES BOTH DURING EMBRYONIC DEVELOPMENT AND FROM EMBRYONIC TISSUE TO TISSUE. SGG IS REQUIRED FOR PHOSPHORYLATION AND WG SIGNAL NEGATIVELY REGILATES ARM PHOSPHORYLATION AND WG SIGNAL NEGATIVELY REGILATES ARM PHOSPHORYLATION HYPOPHOSPHORYLATID FORM OF ARM INCREASES IN STEADY-STATE LEVELS.

-!- SIMILARITY: CONTAINS 12.5 ARM REPEATS.
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 PROSITE; PS50176; ARM_REPEAT; 9.

Developmental protein; Segmentation polarity protein; Repeat;
Cell adhesion; Cytoskeleton; Structural protein; Phosphorylation;
Alternative splicing.
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Callister D.M., Campbell L.A., Darlamitson A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C. Glover D.M.
 "From sequence to chromosome: the tip of the X chromosome of D.
 ASP/GLU-RICH (ACIDIC)
 EMBL; AF001213; AAB58731.1; EMBL; AE001213; AAF45688.1; ALT_INIT. EMBL; AL021106; CAA15946.1; JOINED. EMBL; AL021086; CAA15946.1; JOINED. EMBL; AL021106; CAA15935.1; EMBL; AL021106; CAA15935.1; JOINED. PIR; A11861; A31861.
 MEDLINE=95113174; PubMed=7529201;
 Pfam; PF00514; Armadillo_seg; 12.
 InterPro; IPR000225; Armadillo.
 EMBL; X54468; CAA38350.1; -.
 Science 287:2220-2222(2000).
 FlyBase; FBgn0000117; arm
 SMART; SM00185; ARM; 11.
 158
200
 T02977
 PHOSPHORYLATION
 melanogaster
 Glover D.M.
 TRANSFAC;
 DOMAIN
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ö
 ASP/GLU-RICH (ACIDIC).
LGPEEAYEGLYGQGPPSVHSSHGGRAFHQGGYDTLPIDSMO
GLEISSPYGGGGAGGARGNGGANGGANGGANGGANGGANGAIPPSGA
PTSPYSMDMDVGEIDAGALNFDLDAMPTPPNDNNNLAAWYD
TDC -> ILYQ (IN NEUFAL ISOFORM).
40DADGFB83163049 CRC64;
 Gaps
 .;
0
 Length 843;
 4; Indels
 438 NNORNKATVCOVGGVDALVRTIINAGDREEITEPAVCALRHLTS 481
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
 ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 10.
ARM 11.
ARM 11.
ARM 11.
ARM 11.
ARM 11.
 Score 187; DB 1;
Pred. No. 6.5e-18;
 7; Mismatches
 MM;
 82.4%;
 Query Match 82.4'
Best Local Similarity 75.0'
Matches 33, Conservative
 496
 647
 843 AA;
 243
3327
3327
4411
450
539
539
6609
648
 SECUENCE
 VARSPLIC
REPEAT
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REPEAT
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01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 01-RAR-2002 (Rel. 41, Last annotation update) Armadillo segment polarity protein. STANDARD; ARM MUSDO ARM\_MUSDO RESULT

Musca domestica (House fly). Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Musca. Peifer M.A., Wieschaus E.;
Peifer M.A., Wieschaus E.;
"The product of the Drosophila melanogaster segment polarity gene armidillo is highly conserved in sequence and expression in the housefly musca domestica.";
J. Mol. Evol. 36:224-233(1993).
-!- FONCTION: SEGMENT POLARITY PROTEIN, MUTATION IN ARM PRIMARILY
-!- FONCTION: OF THE FOSTERIOR PART OF THE SEGMENT AND LEAD TO THE
--- APPEDDICTION OF ANTERIOR STRUCTURES WITHIN THIS REGION. MAY BIND
--- AP-CADHERINIAND PARTICIPATE IN THE TRANSMISSION OF DEVELOPMENTAL SEQUENCE FROM N.A. NCBI\_TaxID=7370;

11. SUBCELLULAR LOCATION: INNER SURFACE OF CELL MEMBRANE. SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. 

entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit is along as its content is in no way modified and this statement is not removed. Usage by and for commercial

Pfam: PF00514; Armadillo\_seg; 12. SMART; SM00185; ARM; 11.

ARM 1

159

REPEAT

IPR000225; Armadillo.

EMBL; L04874; AAA29292.1; -.

HSSP; 002248;

InterPro;

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Gaps

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NiMatch 1, 1, 75.3%; Score 171; DB 1; Length 820; Local Similarity .68.2%; Pred. No. 1e-15; hes g 30; Conservative 11; Mismatches 3; Indels
 57255E0F57795FD3 CRC64;
 ANYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 8.7.6
 ARM
ARM
ARM
ARM
ARM
ARM
 MGD; MGI:9650; Jup.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
 (Rel. 34); Created)
 89361 MW;
 EMBL; M90365; AAB02885.1; -.
 [2]
REVISIONS TO 294 AND 296.
 STANDARD;
 SMART; SM00185; ARM; 8.
 Mus musculus (Mouse)
 820. AA;
 SEQUENCE FROM N.A:
 100W
 HSSP; r Q02248;
 01-JUL-1993
 $35092
 PLAK_MOUSE
 Query, Match
 SEQUENCE
 REPEAT
REPEAT
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REPEAT
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 PLAK_MOUSE
 Matches
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 ö
 Gaps
 in two invertebrates, Urechis caupo and Tripneustes gratilla.";
Blochim. Blochim. Brophys. Acta 1173:337-341(1993).
-!- FUNCTION: BINDS TO THE CYPOLASMIC DOMAIN OF THE CELL-CELL
ADHESION WOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CAPTENINS TO CAPHERINS PRODUCES A
COMPLEX WHICH IS LINED TO THE ACTIN FILAMENT NETWORK, AND
WHICH
SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
 Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
 'Identification of homologues to beta-catenin/plakoglobin/armadillo
 ö
 Segmentation polarity protein; Repeat;
 Length 813;
 Indels
 PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
 73E61F59BDBFA580 CRC64;
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
 SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
 Structural protein. ASP/GLU-RICH (ACIDIC)
 4
 Score 184; DB 1;
Pred. No. 1.6e-17;
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 820 AA
 8; Mismatches
 Tripneustes gratilla (Hawaian sea urchin).
 SIMILARITY: CONTAINS 10 ARM REPEATS
 or send an email to license@isb-sib.ch)
 ARM 1.
ARM 2.
 MEDLINE=93305730; Pubmed=8318544;
 Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 12.
 ARM
ARM
ARM
ARM
ARM
ARM
ARM
PROSITE; PS50176; ARM_REPEAT; 9.
 HSSP; Q02248; 1DOW.
InterPro; IPR000225; Armadillo.
 88237 MW;
 EMBL; L10354; AAA30089.1; -.
 81.18;
illarity 72.78;
Conservative
 STANDARD;
 Developmental protein;
 221
262
304
387
427
 S33794; S33794.
 Query Match
Best Local Similarity
Matches 32; Conserv
 813 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=7673;
 349
388
430
 Rosenthal E.T.;
 PROPERTIES
 Cell adhesion;
 Beta-catenin.
 Tripneustes
 CTNB_TRIGR
 SEQUENCE
 REPEAT
REPEAT
REPEAT
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 REPEAT
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 CTNB_TRIGR
 KKW
KKW
KKW
FTT
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FTT
FTT
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 -1-: SUBUNIT: HOMODIMER.
-1-: SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
": ASSOCIATED FORM...
 MEDLINE-92376536; PubMed-1509266; Butz. S., Stappert J., Weissig H., Kemler R.; "Plakoglobin and beta catenin: distinct but closely related."; Science 257:1142-1144(1992).
 PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
 -1-; SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
 01-0cT-1996 (Rel. '34') Last sequence update)
01-MAR-2002 (Rel.:41, Last annotation update)
Junction plakoglobin (Desmoplakin III) (Fragment).
621 AA
PRT;
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the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or/send an email to license@lsb-sib.ch).
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
 Gaps
 DEF. BIO1. 153:337-346(1992).

-1'- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
SYNCTIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOGLOBIN IN BOTH THE DESNOSMES AND IN THE
INTERNEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRUCTURE AND FUNCTION OF SUBMEMBRANDUS PLAQUES.
 MEDLINE-93093332; PubMed-1459359;
Fouquet B., Zimbelmann R., Franke W.W.;
Lightification of plakoglobin in occytes and early embryos of
Xenopus leevis: maternal expression of a gene encoding a junctional
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III).
Xenopus laevis (African clawd frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 GQLA -> DSSL (IN REF. 1; AAA64895).
V -> A (IN REF. 1; AAA64895).
472741F400D388FD CRC64;
 SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
 ;
 de Marais A.A., Moon R.T.; "The armadillo homologs beta-catenin and plakoglobin are differentially expressed during early development of Xenopus
 Length 743;
 Ouery, Match 73.1%; Score 166; DB 1; Length 74 Best Local Similarity 68.2%; Pred. No. 4.4e-15; Matches 30; Conservative 7; Mismatches 7; Indels
 - SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
 44
 . 1 NYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 419 NNSKNKTLVYQNSGVEALIHAILRAGDKDDITEPAVCALRHLTS
 738 AA
 PROBABLE
 ARM 1.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
 PRT;
 SEQUENCE OF 133-292 FROM N.A. MEDLINE-93012479; PubMed-1397690;
 plague protein.";
Differentiation 51:187-194(1992).
 ₩.
 81498
 STANDARD;
 521
 Xenopodinae; Xenopus.
 ASSOCIATED FORM.
 SEQUENCE FROM N.A.
 743 AA;
 NCBI_TaxID=8355;
 PLAK_XENLA
INIT_MET
 CONFLICT
CONFLICT
SEQUENCE
 RESULT 11.
 laevis.
 REPEAT
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 ö
 Gaps
 MEDLINE-89264555; PubMed-2726765; Pranke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M., Schiller D.L., Cowin P.; "Molecular cloning and amino acid sequence of human plakoglobin, the
 common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989)
-!- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE
INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
 ;
0
 Length 621;
 Indels
 PROSITE; PSS0176; ARM_REPEAT; 8.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
 ARM 1.
ARM 3.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 7.
ARM 9.
17CF444607422BAA CRC64;
 44
 -!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 Pred. No. 3.6e-15; 7; Mismatches 7:
 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III).
JUP OR DP3.
 743 AA
 PRT;
 ARM
ARM
ARM
ARM
ARM
ARM
 Pfam; PF00514; Armadillo_seg; 10.
SMART; SM00185; ARM; 8.
 7;
 InterPro; IPR000225; Armadillo.
 68111 MW;
 73.18;
68.28;
 EMBL; M23410; AAA64895.1; -.
 Conservative
 STANDARD;
 SUBUNIT: HOMODIMER
 A32905; A32905.
 Homo sapiens (Human)
 ASSOCIATED FORM
 ¥
 Local Similarity
nes 30; Conserv
 [1]
SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 MIM; 173325;
 PLAK_HUMAN
 SEQUENCE
 Query Match
 NON_TER
REPEAT
 RPEAT
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 Matches
 HUMAN
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 STANDARD;
 (Rel. 41, 1
 SEQUENCE FROM N.A. . . .
 Homo sapiens (Human).
 Cytoskeleton; Repeat.
REPEAT 377
 SEQUENCE FROM N.A.
 578 AA;
 Best Local Similarity
Matches 11; Conserv
 SEQUENCE FROM N.A.
 TISSUE=Placenta;
 NCBI_TaxID=9606;
 01-MAR-2002
 01-MAR-2002
01-MAR-2002
 Plakophilin
 Franke W.W.
 PKP3_HUMAN
 SEQUENCE
 Query Match
 protein.
 REPEAT
 REPEAT
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 REPEAT
 13
 PKP3_HUMAN
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 Gaps
 STRAIN=S28BC / AB972;
STRAIN=S28BC / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Schl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
 -1- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. MOST SIMILAR TO PLAKOGLOBINS.
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 Wang Y.X., Catlett N.L., Weisman L.S.;
Unpublished observations (XXX-1997).
-!- FUNCTION: FUNCTIONS IN BOTH VACUOLE INHERITANCE AND PROTEIN
TARGETING FROM THE CYTOPLASM TO VACUOLE.
 ;
0
 Length 738;
 Indels
 Structural protein; Repeat. ARM 1.
 -> V (IN REF. 2).
-> T (IN REF. 2).
569DBE69D08BBC58 CRC64;
 44
 67.0%; Score 152; DB 1; Le co 1%; Pred. No. 3.7e-13; 8;
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Vacuolar protein 8.
VAC8 OR YEL013W.
 578 AA
 -!- SIMILARITY: CONTAINS 9 ARM REPEATS.
 ARM 2.
ARM 3.
ARM 5.
ARM 6.
ARM 7.
ARM 9.
 PRT;
 InterPro; IPRO00225; Armadillo.
Pfam: PF00514; Armadillo_seg; 11.
PRO8TIF; PS00116; ARM; ID.
PROSTIF; PS00176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Stru
 81711 MW;
 Query Match
Best Local Similarity 59.1%;
Matches 26; Conservative 1
 EMBL; X67078; CAA47463.1;
PIR; S24636; S24636.
PIR; S35093; S35093.
 EMBL; M95593; AAA49931.1;
 STANDARD;
 738 AA;
 HSSP; Q02248; 2BCT
 CHARACTERIZATION
 NCBI_TaxID=4932;
 VAC8_YEAST
P39968;
 SEQUENCE
 CONFLICT
 CONFLICT
 REPEAT
REPEAT
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REPEAT
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 REPEAT
 REPEAT
 REPEAT
 VAC8_YEAST
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 Gaps
 MEDLINE-99310799; Pubmed-10381383;
Bonne'S., van Hengel J., Nollet F., Kools P., van Roy F.;
"Plakophilin-3, a novel armadillo-like protein present in nuclei and
 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: MAY PLAY A ROLE IN JUNCTIONAL PLAQUES.

-!-FUNCTION: MAY PLAY A ROLE IN JUNCTIONAL PLAQUES.

-!-: SUBCELLULAR LOCATION: Nuclear and associated with desmosomes.

-!-: STRATFRIED SPECIFICITY: FOUND IN DESMOSOMES OF MOST SIMPLE AND CARRATERED RETHELIA. NOT FOUND IN FOREKIN FIBROBLASTS AND VARIOUS SARCOMA-DERIVED CELL LINES. BESIDE DENRIFIC RETICULAR CELLS OF LYMPHATIC FOLLICLES NOT FOUND IN NON-EPITHELIAL

DESMOSOME-BEARING TISSUES.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 .;
7
 TISSUE=Colon carcinoma;
MEDLINE=99302495; PubMed=10374265;
Schmidt A., Langbein L., Praetzel S., Rode M., Rackwitz H.-R.,
 Plakophilin 3 - a novel cell-type-specific desmosomal plaque
 Length 578;
 Indels
 B2E75774B47E5933 CRC64;
 44
 -: SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
 14;
 2 NYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 DB 1;
1.3;
 Last sequence update)
Last annotation update)
 Æ
 Mismatches
 797
or send an email to license@isb-sib.ch)
 Score 60;
Pred. No.
 ARM 1.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 9.
 PRT;
 desmosomes of epithelial cells.";
J. Cell Sci. 112:2265-2276(1999).
 Differentiation 64:291-306(1999).
 SGD; SO000739; VAC8. :
InterPro; IPR000225; Armadillo.
InterPro; Armadillo.seg; 9.
SMART; SM00185; ARM; 8.
PROSITE: PS50176; ARM_REPEAT; 7.
 26.4%; Scc
25.6%; Pre
tive 16;
 (Rel. 41, Created)
 63207 MW;
 EMBL; U18530; AAB64490.1; -.
 Conservative
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(See http://www.isb-sib.ch/announce/
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
 MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 Pram: PF00689; Cation_ATPase_C; 1.
Pram: PF00690; Cation_ATPase_C; 1.
Pram: PF00122; E1-E2_ATPase, 1.
Pram: PF00129; Hydrolase; 1.
Privis: PR00119; CATATPASE_E1_E2; 1.
PROSITE; PS00154; ATPASE_E1_E2; 1.
Hydrolase; Calcium transport; Transmembrane; Phosphorylation;
 EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
ATP (BY SIMILARITY).
 23.8%; Score 54; DB 1; Length 1011; 31.7%; Pred. No. 16; ive 9; Mismatches 15; Indels
 4F2103FED2A7D5D0 CRC64;
 Smith D.R., Robison K., Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
 Usage by
 EXTRACELLULAR (POTENTIAL)
 EXTRACELLULAR (POTENTIAL)
 EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 14.007, 01-007-1995 (Rel. 32; Created) 01-007-1995 (Rel. 32; Last sequence update) 01.007-1995 (Rel. 32; Last sequence update) 16.0C7-2001 (Rel. 40, Last annotation update) Putative AAA-family Arpase Mil316.
Mil316 OR MicB2333.12 OR A2126A OR B2126_C1_167.
 609 AA.
 modified and this statement is not removed.
 or send an email to license@isb-sib.ch)
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.
 Interpro; IPR001757; E1-E2 ATPase
Interpro; IPR001454; Hydrolase.
Interpro; IPR000661; Na_H_K_ATPase.
 InterPro; IPR004014; Cation_ATPase.
 110313 MW;
 EMBL; M73769; AAA30227:1; -.
 entities requires ajlicense
 Query Match
Best Local Similarity 31.77
Matches 13; Conservative
 STANDARD;
 PIR; A45598; A45598.
 Magnesium; ATP-binding
 Mycobacterium leprae.
 1011 AA;
 HSSP; 'P04191; 1EUL
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 YL15_MYCLE
P46509;
 STRAIN-TN;
 DOMAIN
TRANSMEM
 TRANSMEM
 TRANSMEM
 FRANSMEM
 FRANSMEM
 FRANSMEM
 FRANSMEM
 PRANSMEM
 SEQUENCE
 MOD_RES
BINDING
 DOMAIN
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 YL15_MYCLE
 RESULT 15
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 3;
 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MAY BE LOCATED IN
 Gaps
 Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
 CATALYTIC ACTIVITY: ATP + H(2)O + CA(2+)(IN) = ADP + PHOSPHATE +
 PROSITE; PS50176; ARM_REPEAT; 1.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
 01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable calcium-transporting ATPase (EC 3.6.3.8) (Calcium pump).
 "Structure and transcription of a P-ATPase gene from Trypanosoma
 FUNCTION: THIS MAGNESIUM-DEPENDENT ENZYME CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE TRANSPORT OF THE CALCIUM
 5,
 THE FLAGELLAR POCKET OF THE MEMBRANE.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES).
 Length 797;
 Indels
 D43C7E77FA805E7E CRC64;
 4 KNKMMVCQVGGIEALVRTV---LRAGDRED-ITEPAICALRHLT 43
 13;
 DB 1;
 8; Mismatches
 PRT; 1011 AA
 Mol. Biochem. Parasitol. 46:241-251(1991).
 Score 58.5;
Pred. No. 3;
SIMILARITY: CONTAINS 8 ARM REPEATS.
 ARM 2.
ARM 3.
ARM 4.
 ARM 6.
ARM 7.
ARM 8.
 MEDLINE=92018021; PubMed=1833643; Revelard P., Pays E.;
 Pfam; PF00514; Armadillo_seg; 4.
SMART; SM00185; ARM; 3.
 EMBL; Z98265; CAB44310.1; -.
EMBL; AF053719; AAF23050.1; -.
EMBL; BC000081; AAH00081.1; -.
 InterPro; IPR000225; Armadillo.
 (Rel. 28, Created)
(Rel. 28, Last seq
 87081 MW;
 25.8%;
 Conservative
 STANDARD;
 390
432
487
 Query Match
Best Local Similarity
 797 AA;
 (BY SIMILARITY)
 SEQUENCE FROM N.A.
 491
596
 CA(2+)(OUT
 01-FEB-1994
 18;
 ATC_TRYBB
P35315;
 SEQUENCE
 Repeat.
 REPEAT
REPEAT
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 REPEAT
 Matches
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 RESULT
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Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Ruther S., Seeger K., Sinon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
 TP (POTENTIAL).
C3AA1691815FC873 CRC64;
 DEPICHEATORY THE ALGORY THE ALGOR
 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
 EMBL; U00017; AAA17185.1; --
EMBL; AAL033310; CAA22926.1; --
EMBL; AL583921; CAC31697.1; --
LEPTOMA; ML1316; --
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Query Match 23.6%; Score 53.5; DB 1; Length 609; Best Local Similarity 36.7%; Pred. No. 11; Matches 11; Conservative 9; Mismatches 9; Indels

Search completed: July 29, 2002, 16:09:56 Job time: 761 sec

| Q9y446 homo sapien<br>Q9fm35 arabidopsis<br>Q9eq99 mus musculu<br>Q92d16 listeria in                                        | Q9c239 neurospora<br>Q9amk1 xanthomonas     | Ografio motorie saxa<br>(091419 pseudomonas<br>087594 streptomyce<br>(097)58 streptomyce                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 099rw4 staphylococ<br>0931g2 staphylococ<br>09erx3 rattus norv<br>093x72 gossypium h | 092551 nomo sapien<br>Q96n94 homo sapien<br>O50202 rhodococcus | Q9uuxi schizosacch<br>Q9misi arabidopsis<br>Q91643 serratia ma | Q22948 caenorhabdi                                | Q901SL nome Saplen<br>Q9u308 caenorhabdi<br>Q9ssj6 arabidopsis | Q959a0 arabhuchsis<br>Q9kgj2 bacillus ha<br>O24128 nicotiana t<br>O81161 carica papa  |                                                          |            |                                  |                                                                                                                                                                         |                                                                                | ; Euteleostomi;<br>i; Ostariophysi;                                                                                                                |                                                                                                                                                         | s in zebrafish occurs following                                                  |                                                                                                            |                                                                                                |                                                                     | 264;                                                                                       | .h 780;                                                        | inders U; Gaps U;                           | 44<br>472                                                      |                     |
|-----------------------------------------------------------------------------------------------------------------------------|---------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------------------------------|----------------------------------------------------------|------------|----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|--------------------------------------------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------|----------------------------------------------------------------|---------------------|
| 17.158.5 25.8797 4 Q9X446<br>18.15.8 57 25.1 165 10 Q9FW35<br>19.77.8 57 25.1 308 11 Q9EQ99<br>20:7.56.5 24.9 381 16 Q92D16 | 24:7 246 3<br>24:2 289 2                    | 24%21838 13<br>24%0393 16<br>24.0581 2<br>24.0588 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 24.0 984<br>24.0 984<br>23.8 268<br>23.8 328                                         | 23.6 : 1113 4<br>23.6 : 591 2                                  | 23:3 564 3<br>23:3 727 10                                      | 23:1 .380. 5                                      | 23:1 1181 5<br>22:9 530 10                                     | 22:9 1181 16<br>22:7 107 10<br>22:7 408 10                                            | 01 01 01 01 01 01 01 01 01 01 01 01 01 0                 | RESULT : 1 | O90424 PRELIMINARY; PRT; 780 AA. | AC 090424;<br>DT 01:NOV-1996 (TrEMBLrel. 01, Created)<br>DT 01:NOV-1996 (TrEMBLrel. 01, Last sequence update)<br>DT 01:DEÇ-2001 (TrEMBLrel. 19, Last annotation update) | -DE B-CATENIN.<br>GN CTWNB:<br>OS Brachydanio rerio (Zebrafish) (Zebra danio). | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; OC Actinopterygii; Neopterygii; Teleostei; Buteleostei OC Cypriniformes; Cyprinidae; Danio. | OX NCBI_TaxID=7955; RN [1]. RP SEQUENCE FROM N.A. RX MEDLINE-96122902: PubMed=8562427;                                                                  | elly'G.M., Erezyilmaz D.F., Moon R.T.;<br>Induction of a secondary embryonic axi | <pre>R1 Lim OverExpression of December; RL Mech.:Dev. 53:261-273(1995). DR EMBL;:U41081; AAC59732.1;</pre> | DR HSBP: P35222; 1G30. DR ZFIN; ZDB-GENE-980526:362; ctnnb. DR InterPro; PPR000225; Armadillo. | DR Pfam; PP00514; Armadillo_seg; 12.<br>DR SMART; SM00185; ARM; 11. | DR PROSITE, PS50176; ARM_REPEAT; 8<br>SQ SEQUENCE 780 AA; 85542 MW; D7A1FB80F94066DC CRC64 | core 227; DB 13;<br>red. No. 1.5e-22;                          | Matches : 44; Conservative U; Mismatches U; | Qy 1 NWYKNKMWYCQVGGIEALWRYLRAGDREDITEPAICALRHLTS 4             |                     |
| 4.5<br>Compugen Ltd.                                                                                                        |                                             | rch time 124.4 Seconds<br>(without alignments)<br>61.188 Million cell updates/sec                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | AGDREDITEPAICALRHLTS 44                                                              |                                                                |                                                                | : 562222                                          |                                                                |                                                                                       |                                                          |            |                                  |                                                                                                                                                                         |                                                                                |                                                                                                                                                    | cted by chance to have a sof the result being printed,                                                                                                  |                                                                                  | Description                                                                                                | Q90424 brachydanio<br>Q9d335 mus musculu                                                       |                                                                     | Q9n144 ciona intes<br>Q25100 hydra magni<br>O61229 lytechins                               | Q15151 homo sapien<br>Q9bwc4 homo sapien<br>P70565 rattus norv | O44326 caenorhabdi                          | 018825 caenorhabdi<br>0912a6 arabidopsis<br>09sttl arabidopsis | .09fjj0 arabidopsis |
| GenCore version 4.5<br>Copyright (c) 1993 - 2000 Compu                                                                      | OM protein - protein search, using sw model | Run on: July 29, 2002, 16:12:09; Search (wild the control of the c | Title: US-09-641-104A-11 Perfect score: 227 Sequence: 1 NNYKNKMMVCQVGGIEALVR         | Scoring table: BLOSUM62<br>Gapop 10.0 , Gapext 0.5             | Searched: 562222 seqs, 172994929 residues                      | Total number of hits satisfying chosen parameters | Minimum DB seq length: 0<br>Maximum DB seq length: 200000000   | Post-processing: Minimum Match 0%<br>Maximum Match 100%<br>Listing first 45 summaries | Database : SPTREMBL_19;*  1: SP_archea:* 2: SP_bateria:* |            | sp_mammal:* sp_mhc:*             | 8: Sp_organeile:*<br>9: Sp_phage:*<br>10: Sp_plant:*<br>11: Sp_rodent:*                                                                                                 |                                                                                | <pre>15: sp_rvirus:* 16: sp_bacteriap:* 17: sp_archeap:*</pre>                                                                                     | Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score discored. | SUMMARIES                                                                        | Result Query<br>No. Score Match Length DB ID                                                               | 227 100.0 780 13<br>227 100.0 781 11                                                           | 227 100.0 781<br>194 85.5 773                                       | 193 85.0 769 5<br>181 79.7 806 5<br>171 75.3 821 5                                         | 8 166 73.1 745 4<br>9 166 73.1 745 4<br>0 159 70.0 745 11      | 2 131 57.7 678 5 (                          | 74 32.6 811 5 0<br>59.5 26.2 825 10<br>58.5 25.8 509 10        | 58.5 25.8           |

090335

RESULT

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 ö
 Ciona intestinalis.
Eukaryota, Metázoa, Chordata, Urochordata, Ascidiacea, Phlebobranchia,
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia; Cionidae; Ciona
 Gaps
 Gaps
 SEQUENCE FROM N.A.

MEDLINE=98443204; PubMed=9769178;

MEDLINE=98443204; PubMed=9769178;

Station of Station of Station of Station of Station of the trunk-tail patterning in the ascidian embryo: a possible interaction of cascades between lithium/beta-catenin and localized maternal factor pem.";

Dev. Biol. 202:264-279(1998).

EMBL; AB012160; BAA327891; --

HSSP; P35222; IGSJ.
 ö
 ö
 Length 781;
 Score 194; DB 5; Length 773;
Pred. No. 4.8e-18;
3; Mismatches 4; Indels
 MEDLINE-97464068; PubMed-9322759;
LUVJ. Chuong C.M., Widelitz R.B.;
"Isolation and characterization of chicken beta-catenin.";
edge 196.201-207(1997);
 Indels
 SWART; SM0185; ARM; 11.
PROSITE; PS50176; ARM_REPEAT; 8.
SEQUENCE 781; AA; 85438 MW; 6D205D9A4DBAC562 CRC64;
 Pfem: PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; 9.
PROSITE; P50176; ARM REBAT; 7.
SEQUENCE 773 AA; 85217 WW; C1340CF82AFEBDAB CRC64;
 430 NNYKNKMMYCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 473
 419. NNMSNKTRVCQVGGIEALVRTVLQAGDREDITEPSVCALRHLTS 462
 44
 44
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 1 NNYKNKMWVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 100.0%; Score 227; DB 13; 100.0%; Pred. No. 1.5e-22;
 773 AA
 769 AA
 0; Mismatches
 STRAIN-WHITE LEGHORN; TISSUE-DORSAL SKIN;
 Created)
 Created)
 PRT;
 PRT;
 Interpro; IPRO0225; Armadillo.
Pfam; PF0014; Armadillo_seg; 12.
SMART; SM00185; ARM! 11
 InterPro; IPR000225; Armadillo.
 85.5%;
cy 84.1%;
 EMBL, U82964, AAB80856:1, -.
 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, BETA-CATENIN.
 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19,
 Best Local Similarity 100.
 Matches 37; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Local Similarity
SEQUENCE FROM N.A.
 NCBI TaxID-51511;
 Ciona savignyi.
 CIBETA-CATENIN.
 BETA-CATENIN.
 Query Match
 Query Match
 076152
 Q9NL44;
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 Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Asdota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aon H., Baldarelli R., Barsh G., Barsh G., Bult C., Fultuno M., Aon H., Baldarelli R., Barsh G., Brownstein M.J. Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Marshia-Baria V., Schick M., Washia-Baria V., Kawaji H., Kohtsuki S.,
 ö
 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
 ö
 Length 781;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE COLON CDNA, RIKEN FULL-LENGITH ENRICHED LIBRARY,
CLONE:9030417H18, FULL INSERT SEQUENCE.
 MCD; MCI:88276; Catnb.
InterPro; IRR000225; Armadillo.
InterPro; IRR000185; Armadillo_seq; 12.
SMART; SMO0185; ARM: 12.
PROSITE; PS50176; ARM_REPEAT; 7.
SEQUENCE 781 AA; 85546 MW; 937538C3B5CD75D1 CRC64;
 Last sequence update)
Last annotation update)
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ilarity 100.0%; Pred. No. 1.5e-22;
Conservative 0; Mismatches 0;
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 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-COLON;
MEDLINE-21085660; Pubmed-11217851;
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 Nature 409:685-690(2001).
EMBL; AK018515; BAB31250.1;
 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
 PRELIMINARY;
 PRELIMINARY;
 Mus musculus (Mouse).
 Query Match
Best Local Similarity
Matches 44; Conserv
 NCBI_TaxID-10090
 Gallus.
NCBI_TaxID=9031;
[1]
 BETA CATENIN.
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042486 042486;

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042486 11D 04400 AAC 04400 DT 011 DDT 
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MEDLINE=96157724, PubMed=8576101;
Ozawa M., Nuruki K.; Toyoyama H., Ohi Y.;
"Cloning of an alternative form of plakoglobin (gamma-catenin) lacking
 SEQUENCE FROM N.A.
MEDLINE-98104237; PubMed-9441670;
MILLE J.R., McClay D.R.;
Miller J.R., McClay D.R.;
Changes in the pattern of adherens junction-associated beta-catenin accompany morphogenesis in the sea urchin embryo.";
Devi: biol. 192:310-322(1997).
EMBL: U34814; ARC06340.1;
EMBL: U34814; ARC06340.1;
 Gaps
 Schiller D.L., Cowin P.; "Molecular cloning and amino acid sequence of human plakoglobin, the
Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
 PubMed=11016852;
Whittock N.V., Eady R.A.J., McGrath J.A.;
"Genomic Organization and amplification of the human plakoglobin
 ö
 SEQUENCE FROM N.A.
MEDLINE-89264555; PubMed=2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
 Length 821;
 Query;Match 75.3%; Score 171; DB 5; Length 8; Best Load Similarity 68.2%; Pred. No. 7.3e-15; Matches 30; Conservative 11; Mismatches 3; Indels
 Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
 PROSIȚE: PSOU687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
PROSIȚE; PSSU176; ARM_REPEAT; 8.
SEQUENCE 821 AA; 89558 MW; 71E21D562A99C5AD CRC64;
 447 NNSRNKMIVSQMAGVEALVQTLMKAGDREEITEPAVCALRHVTS 490
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS 44
 Last sequence update)
Last annotation update)
 common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989)
 Ą
 Interpro, IPR002086; Aldehyde_dehydr.
Interpro; IPR000225; Armadillo.
 Created)
 PRT;
 Pfám; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 12.
 Exp. bermatol. 9:323-326(2000).
EMBL; z68228; CAA92522.1; -.
 the fourth armadillo repeat.";
J. Biochem. 118:836-840(1995).
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 SEQUENCE OF 239-409 FROM N.A.
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17, PLAKOGLOBIN.
 PRELIMINARY;
 Homo sapiens (Human).
 [4],
SEQUENCE FROM N.A.
 SECUENCE FROM N.A.
 NCBI_TaxID=7654;
 TISSUE-PLACENTA;
 NCBI_TaxID=9606;
 Q15151 PR
Q15151; Q15093
 Zimbelmann R.;
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 Imai K., Takada N., Satoh N., Satou Y.;
"An essential role of beta-catenin in the endoderm specification of ascidian embryo.";
Submitted (AuG-1999) to the EMBL/GenBank/DDBJ databases.
HSSP; P35222; 1G3J.
 ő
 Hydra magnipapillata (Hydra).
Bukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
 ;
 SEQUENCE FROM N.A.
STRAIN=WILDTYPE 105;
MEDLINE=96257271; PubMed=8654977;
Hobmayer E., Hatta M., Fischer R., Fujisawa T., Holstein T.W.,
 Score 181; DB 5; Length 806;
Pred. No. 3.1e-16;
6; Mismatches 4; Indels
 Length 769;
 Score 193; DB 5; Length 76
Pred. No. 6.6e-18;
2; Mismatches 5; Indels
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689E5E982CD5051A CRC64;
 F61CC489B436E1BC CRC64;
 420 NNMSNKTRVCQVGGIEALVRTVLQAGDREDITEPTVCALRHLTS 463
 44
 44
 01-AUG-1998 (TrEMBLrel. 07, Created)
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 1 NNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTS
 "Identification of a Hydra homologue of the beta-
catenin/plakoglobin/armadillo gene family.";
Gene 172:155-159(1996).
EMBL; U36781; AAC47137.1; --
HSSP; Q02248; 2BCT.
 806 AA
 PRT;
 InterPro; InterP
 InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; II.
PROSITE; PS60176; ARM_REPEAT; 6.
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77.38;
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Best Local Similarity 77.3
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 NCBI_TaxID=6085;
 NCBI_TaxID=7719;
 Cionidae; Ciona
 BETA-CATENIN,
 BETA-CATENIN
 Sugiyama T.;
 225100;
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Umekita Y., Liao §:;.
"Molecular cloning and sequencing of the rat plakoglobin cDNA.";
 Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 STRAIN-SPRAGUE DAWLEY; TISSUE-VAGINA;
 STRAIN-SPRAGUE-DAWLEY; TISSUE-VAGINA;
 SEQUENCE FROM N.A.
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 Hilpakka R.A.
Submitted (MA
 044326;
 RESULT 11
Q9PVF7
ID Q9PVF7
 Q9PVF7;
 RESULT 12
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ID 044326
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0
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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 ;
 Length 745;
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 Indels
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TISSUE-LUNG CARCINOMA;
Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 ted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
BC000441; AAH00441.1; -.
BC011865; AAH11865.1; -.
 HSSP; Q02248; 2BCT.
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Last annotation update)
 Last sequence update)
Last annotation update)
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Best Local Similarity 68.2%; Pred. No. 3.2e-14;
Matches 30; Conservative 7; Mismatches 7;
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Best Local Similarity 68.2%; Pred. No. 3.2e-14;
Matches 30; Conservative 7; Mismatches 7;
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 EMBL; AF233882; AAG16727.1; -. EMBL; AF233882; AAG16727.1; JOINED.
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TISSUE-PLACENTA, CHORIOCARCINOMA;
Strausberg R.;
D50808; BAA09435.1; -.
 01-JUN-2001 (TremBirel, 17, 01-JUN-2001 (TremBirel, 17, 01-DEC-2001 (TremBirel, 19, JUNCTION PLAKOGLOBIN,
 01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19,
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 Homo sapiens (Human)
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 Q9BWC4
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 SEQUENCE FROM N.A.
MEDLINE=99386700; PubMed=10456847;
Cerda, J., Reidenbach S., Pratzel S., Franke W.W.;
Cadherin-catenin complexes during zebrafish oogenesis: heterotypic junctions between oocytes and follicle cells.";
Biol.' Reprod. 61:692-704(1999).
EMBL; AF099738; AAD56592.1; -.
 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Euteleostei; Ostarlophysi;
Cypriniformes; Cyprinidae; Danio.
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 Length 745;
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 1058658; AAB06317.1; -.
HSSP; 105248; 2BCT.
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01:MAY-2000 (TrEMBLiel. 13, Last sequence update)
01:DEC-2001 (TrEMBLiel. 19, Last annotation update)
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 70.0%; Score 159; DB 11; 165.9%; Pred. No. 2.9e-13; 1ive 7; Mismatches 8;
 Ouery'March 65.2%; Score 148; DB 13; Best Local Similarity 59.1%; Pred. No. 9.2e-12; Matches 26; Conservative 8; Mismatches 10;
 729 AA.
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 PRT;
 HSSP; Q02248; 1DOW.
ZFIN; ZDB-GRNE-991207-22; jup.
IntcrPro; IPRO00225; 'Armadillo.
Pfam; PF00514; 'Armadillo_seg; 11.
SMART; SM00185; ARM; 8.
 PROSITE; PS50176; ARM: REPEAT; 8. SEQUENCE 729 AA; 80033 MW; 9
 Query.Match
Best Local Similarity 65.3.
The 29, Conservative
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Arabidopsis thaliana (Mouse-ear cress).
Būkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spērmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
 409: NNRHNKEFMCGNNGVVILVRALTIATKEMGDLRDKEAQQMEDYIESLICTLRHL 462
 Eisenmann D.M., Maloof J.N., Simske J.S., Kenyon C., Kim S.K.; Submitted (MAY:1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 1446673; AAC48154.1; -.
EMBL; AR063846; AAC17424.1; -.
 . I NNYKNKMMVCQVGGIEALVRTVLRA----GD------REDITEPAICALRHL 42
 Length 825;
 SEQUENCE FROM N.A.
Choisne N., Robert C., Brottier P., Wincker P., Cattolico L.,
 SECUENCE FROM N.A.
Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 Score 74; DB 5; Length 811;
Pred. No. 0.14;
3; Mismatches 18; Indels
 Indels
 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162873; CAB85524.1; -.
 92091 MW; A80717BD5971F144 CRC64;
 97D6FFDE71BDFDFF CRC64;
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Spermatophyta; Magnoliophyta; eudicotyledons; core e
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 55.1 KDA PROFEIN.
 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) HYPOTHETICAL 92.1 KDA PROTEIN.
 Score 59.5; DB 10;
Pred. No. 14;
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38.9%;
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Matches 21, Conservative
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 09STT1;
 Q9LZA6;
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09STT1
 09LZA6
 RESULT 15.
 RESULT 14
Q9LZA6
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 Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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Rhabditidae; Peloderinae; Caenorhabditis.
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 Length 678
 Indels
 STRAIN-N2 BRISTOL,
Costa M., Raich W., Agbunag C., Hardin J., Priess J.R.,
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AR016853; AAB94552.1; -.
EMBL; 281564; CAB04572.1; -.
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 Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
 E6C7ED51F6241232 CRC64;
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Last annotation update)
 Last sequence update)
Last annotation update)
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MEDLINE-94150718; PubMed-7906398;
 8;
 InterPro; IPR000225; Armadillo.
 Pfam; PF00514; Armadillo_seg;
PROSITE; PS50176; ARM_REPEAT;
 01-NOV-1996 (TrEMBLrel. 01, C
01-JUN-1998 (TrEMBLrel. 06, L
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C54D1.6 PROTEIN.
C34D1.6 OR BAR-1.
Caenorhabditis elegans.
 74510 MW;
 57.78;
54.58;
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 01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
 Nature 368:32-38(1994).
 Caenorhabditis elegans.
 678 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
 [3]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 HMP-2 OR K05C4.6.
 NCBI_TaxID=6239;
 Harris B.
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 elegans.
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Artiquenave F., Saurin W., Weissenbach J., Mewes H.W., Mayer K.F.X., Lemcke.K., Schueller C., Quetier F., Salanoubat M.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 Gaps
 1;
 Query Match 25.8%; Score 58.5; DB 10; Length 509; Best Local Similarity 35.0%; Pred. No. 12; Matches 14; Conservative 10; Mismatches 15; Indels 1
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO49746; CAB41865.1;
InterPro; IPR000225; Armadillo.
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SMART; SM00185; ARM; 3.
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PROSITE; PS50176; ARM, REPEAT; 1.
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 4 KNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLT 43
 [2]
SEQUENCE FROM N.A.
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Propionibacterium
Propionibacterium
ORF encoded by exo
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Aspergillus nidula
Aspergillus nidula
Novel human diagno
Arabidopsis thalia
Rice pyruvate orth
Recombinant cold-r

F. bidentis pyruva Recombinant cold-r F. brownii cold re Arabidopsis thalia Arabidopsis thalia Human extracellula Human nervous syst

nervous syst human diagno

Novel

Drosophila melanog Human polypeptide HIV-1 strain YBF30 Amino acid sequenc Pseudomonas mendoc Amino acid sequenc

Human colon cancer

Amino acid sequenc Drosophila melanog Drosophila melanog

Human brain expres

Title: Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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New antisense compounds targeting nucleic acids encoding human beta catenin (HBC) useful for treating diseases associated with HBC expression and as prophylaxis to prevent or delay infection,
 Beta catenin; cadherin; metastasis; cadherin-associated protein; human; colorectal cancer; melanoma; antisense oligonucleotide; gene therapy.
 ALIGNMENTS
 AAU53394
AAU60457
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 AAY02610
AAB98023
AAB84207
AAB53336
 AAR76707
AAR90923
AAR76711
AAR90927
 AAM65659
ABB59044
AAO01902
 AAR76710
AAR90926
 AAW68475
 AAW17066
 ABB57962
 AAB07290 standard; .Protein; 781 AA
 99US-0344519
 99US-0344519
 (first entry)
Bennett CF, Cowsert LM;
 (ISIS-) ISIS PHARM INC
 WPI; 2000-410651/35.
 Human beta catenin.
 N-PSDB; AAA58320.
 Homo Sapiens.
 US6066500-A.
 25-JUN-1999;
 01-NOV-2000
 25-JUN-1999;
 23-MAY-2000.
AAE07290;
 AAB07290
 RESULT
 THE STATE OF THE S
 Human beta catenin
Human beta-catenin
Novel human secret
Human beta-catenin
Mouse beta-catenin
Novel human secret
Human beta-catenin
 Drosophila melanog
Drosophila melanog
Drosophila melanog
Human prostate can
 1. \SIDSI\gcgdata\hold-geneseg\genesegp-embl\AA1980.DAT:*
2. \SIDSI\gcgdata\hold-geneseg\genesegp-embl\AA1981.DAT:*
3. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
4. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
4. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
5. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
5. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
6. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
7. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
7. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
8. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
9. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1981.DAT:*
110. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
111. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
112. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
113. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
114. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
115. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
116. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
117. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
118. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
119. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
119. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
119. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
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119. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
120. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
121. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
122. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
123. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
124. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
125. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
126. \SIDSI\gcgdata\hold-geneseq\genesegp-embl\AA1991.DAT:*
127. \SIDSI\gcgdata\hold-geneseq\geneseqq\geneseqq-geneseqq\geneseqq-geneseqq\geneseqq-gen
 July 29, 2002, 16:07:57; Search time 158.47 Seconds (without alignments) 32.242 Million cell updates/sec
 the number of results predicted by chance to have a : than or equal to the score of the result being printed, and by analysis of the total score distribution.
 Description
 US-09-641-104A-12
241
1 RHQEAEMAQNAVRLHYGLPV......PPSHWPLIKATVGLIRNLAL
 4.5
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 747574 seqs, 111073796 residues
 GenCore version
Copyright (c) 1993 - 2000
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 AAY70740
AAU28118
AAE06038
AAU28306
AAU28306
ABB60196
ABB60196
ABB65821
AAB56810
 protein search, using sw model
 AAB07290
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 A_Geneseq_032802:*
1: /SIDS1/qcqdata/
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 1222222222
 DB
 781
781
781
781
781
800
45
840
840
840
 Length
 Pred. No. is the n
score greater than
and is derived by
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Query Match

Score

ν Θ Result

100.0 100.0 100.0 100.0 100.0 93.6 80.9 80.9 80.9

241 241 241 241 241 225.5 195 195 190

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Gaps

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beta-catenin protein. Dominant negative mutants of beta-catenin lack one or more armidillo-like repeats which participate in cadherin binding. Other-mutants include:those lacking amino acids 555-781 or 424-781, or $12.0 f beta-catenin.
 and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for
 The invention relates to novel isolated human secreted polypeptides (I)
 Ren F, Ma Y, Zhou P;
R, Xue AJ, Wang J;
 Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; ostooporosis; bone degenerative disorder; periodontal disease; gut. protection, lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders
 ö
 Length 781;
 Indels
 (d. RHQEAEWAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 100.0%; Score 241; DB 21;
100.0%; Pred. No. 1.6e-26;
ative 0; Mismatches 0;
 Xu C, Wehrman T,
F, Zhang J, Chen
 Novel human secretory protein, Seq ID No 287
 Example 4; SEQ ID No 287; 107pp; English.
 fertility; analgesic; pain; antigen.
 Ā
 AAU28118 standard; Protein; 781
 Liu C, Asundi V, Xu
Yang Y, Drmanac RT,
 07-MAR-2000; 2000US-0519705.
19:MAY-2000; 2000US-0574454.
 17-JUN-2000; 2000US-0596193.
14-JUL-2000; 2000US-0616847.
19-SEP-2000; 2000US-0665363.
20-OCT-2000; 2000US-0693267.
 05-MAR-2001; 2001WO-US04942
 18_DEC-2001 (first entry)
 Best Local Similarity 100.
Matches: 46; Conservative
 WPI; 2001-589934/66.
 (HYSE-) HYSEQ INC.
 Local Similarity
 781; AA;
 N-PSDB; AAS45018
 WO200166689-A2:
 sapiens.
 13-SEP-2001.
 Sequence
 AAU28118;
 Zhao QA,
 Query' Match
us-09-641-104a-12.rag
 Tang
 Homo
 AAU28118
 RESULT
 THE STATE OF THE S
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 The patent discloses a method of female primate contraception comprising administering an antaqonist of a Wnt polypeptide, inhibiting occyte development. Wnt polypeptides are useful for promotive maturation of an immature occyte. Wnt polypeptides are also useful for increasing the number of mature occytes and to enhance occyte viability. Soluble fragments of Wnt polypeptides have the ability to inhibit Wnt signalling, e.g., by blocking binding of a naturally-occurring Wnt protein to its receptor. They may be used to generate monoclonal antibodies which can inhibit occyte development. The present sequence is the human
 Human beta-catenin; Wnt antagonist; contraceptive; contraceptive vaccine; oocyte development; female primate contraception; oocyte viability; monoclonal antibody; Wnt signalling.
 Beta catenin is a member of the catenin family of cytosolic proteins and a key member of the Mnt signalling pathway. Catenins interact with the cytoplasmic domains of cadherin glycoproteins, and are important in maintaining cell adhesiveness. The loss of cell adhesiveness is implicated in metastasis. Beta catenin is also known as cadherin-associated protein and is implicated in colorectal cancer and melanoma. The present sequence is the human beta catenin protein. The coding sequence of this protein was used in the present invention to design antisense oligonucleotides (AAA58327-A588366). The oligonucleotides are capable of human beta catenin. The order to inhibit expression of human beta catenin. The order to inhibit expression of human beta catenin. The oligonucleotides may be used in gene therapy for colorectal cancer or melanoma.
 Contraceptive composition for inhibiting oocyte development in a female primate comprises a Wnt polypeptide antagonist
 Gaps
 ;
0
 Length 781;
 Indels
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 Query Match
100.0%; Score 241; DB 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 46; Conservative 0; Mismatches 0;
 Columns 45-52; 35pp; English.
 AAY70740 standard; protein; 781 AA.
 Example 3; Page 26; 57pp; English.
 inflammation or tumor formation
 Vaino S;
 98US-0104355.
 (first entry)
 (HARD) HARVARD COLLEGE.
 Parr BA,
 WPI; 2000-317845/27
 Human beta-catenin.
 781 AA;
 WO200021555-A1.
 Homo sapiens
 15-OCT-1998;
 13-OCT-1999;
 24-JUL-2000
 Mcmahon AP,
 20-APR-2000
 AAY70740;
 Sequence
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beta-catenin in the cell -

The property of the treatment of central and practices of the property of central and praintissue and its useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, in admyortrophic lateral celerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid cor lymphoid cell disorders, platelet disorders such as thrombooytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporoxis, osteobarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, ceperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, creactions and conditions, such as asthma or other respiratory problems. Creactions and conditions, such as asthma or other respiratory problems. Creactions and conditions, such as asthma or other respiratory problems. Creactions fatt, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune each protein amino acid sequences of the invention. creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of neural and brain tissue and is useful for the treatment of central and amino acid sequences of the invention. 781 AA; Sequence 

; 0 Gaps 0; 100.0%; Score 241; DB 22; Length 781; 100.0%; Pred. No. 1.6e-26; 0; Indels Mismatches ó; 46; Conservative \*Query Match Best Local Similarity Matches

1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46 οy g

AAE06038

AAE06038 standard; Protein; 781 AA.

AAE06038;

25-SEP-2001 (first entry)

Human beta-catenin protein #1.

Human; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient; signalling pathway; beta-catenin. 

Homo sapiens.

WO200152649-A1.

26-JUL-2001

17-JAN-2001; 2001WO-US01459

18-JAN-2000; 2000US-0176786

(STRD ) UNIV LELAND STANFORD JUNIOR.

Weissman IL; Nusse R, Reya T,

WPI; 2001-465328/50.

N-PSDB; AAD11164.

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producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of
In vitro expansion of mammalian stem or progenitor cells, useful for
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The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the

Disclosure; Page 28-30; 33pp; English.

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ö
 or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful, for culturing stem cells and progenitor cells, which retain their pluripotential phenotype after expansion, in vitro. The expanded cell populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoietic function to autologous or
 The present invention relates to a method for in vitro expansion of mammalian stem or progenitor cells, which comprising increasing the intracellular concentration of beta-catenin in a progenitor or stem cell in an in vitro culture medium for a period sufficient for the progenitor
 allogeneic recipients. The present sequence is human beta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway initiated by Wnt proteins, which are mediators of several developmental
 In vitro expansion of mammalian stem or progenitor cells, useful for producing cells that retain their pluripotential phenotype after expansion for use in transplantation, involves increasing the levels of
 Mouse; stem cell culturing; progenitor cell; pluripotential phenotype; transplantation; haematopoietic function; allogeneic recipient; signalling pathway; beta-catenin.
 Gaps
 ő
 Length 781;
 Indels
 1 RHQEAEMAQNAVKLHYQLPVVVKLLHPPSHWPLIKATVCLIRNLAL 46
 100.0%; Score 241; DB 22; 100.0%; Pred. No. 1.6e-26;
 0; Mismatches
 Disclosure; Page 23-24; 33pp; English.
 (STRD)) UNIV LELAND STANFORD JUNIOR
 AAE06039 standard; Protein; 781
 Reya T, Nusse R, Weissman IL;
 Mouse beta-catenin protein #2.
 17-JAN-2001; 2001WO-US01459.
 18-JAN-2000; 2000US-0176786.
 25-SEP-2001 (first entry)
 Matches , 46; Conservative
 beta-catenin in the cell
 Sequence 781 AA;
 WPI; 2001-465328/50.
 Query Match
Best Local Similarity
 N-PSDB; AAD11165.
 WO200152649-A1.
 Mus musculus.
 26-JUL-2001.
 processes.
 AAE06039;
 AAE06039
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intracellular concentration of beta-catenin in a progenitor or stem cell in an in vitro culture medium for a period sufficient for the progenitor or stem cell to divide. The number of cells having the functional phenotype of the stem or progenitor cells is expanded. The method is useful for culturing stem cells and progenitor cells, which retain their populations are useful as a source of stem cells, which retain their populations are useful as a source of stem cells, e.g. to reconstitute function in a host that is deficient in a particular cell lineage or lineages. The expanded cell populations are also useful in transplantation to restore haematopoietic function to autologous or allogeneic recipients. The present sequence is mouse beta-catenin protein. Beta-catenin is a pivotal player in the signalling pathway initiated by Wnt proteins, which are mediators of several developmental
 Zhou P;
 ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
 Gaps
 Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders
 Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 Xu C, Wehrman T, Ren F, Ma Y, Zhou
', Zhang J, Chen R, Xue AJ, Wang J;
 ·,
 100.0%; Score 241; DB 22; Length 781; 100.0%; Pred. No. 1.6e-26; tive 0; Mismatches 0; Indels 0;
 474 rhqeaemaqnavrlhyglpvvvkllhppshwplikatvglirnlal 519
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 Novel human secretory protein, Seq ID No 663.
 AAU28306 standard; Protein; 800 AA.
 Drmanac RT,
 2000US-0574454.
2000US-0596193.
2000US-0616847.
 05-MAR-2001; 2001WO-US04942.
 Asundi V,
 2000US-0519705
 2000US-0665363
2000US-0693267
 18-DEC-2001 (first entry)
 Query Match
Best Local Similarity 100.
Matches 46; Conservative
 WPI; 2001-589934/66.
 Liu C, A
Yang Y,
 Sequence 781 AA;
 (HYSE-) HYSEQ INC
 N-PSDB; AAS45206
 WO200166689-A2.
 14-JUL-2000;
19-SEP-2000;
20-OCT-2000;
 Homo sapiens.
 07-MAR-2000;
 19-MAY-2000;
17-JUN-2000;
 13-SEP-2001
 processes.
 AAU28306;
 rang YT,
 QA,
 9
 Zhao
 AAU28306
 RESULT
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The figuration fellers to move I solated human secreted polypeptides (I) and and (II) are useful for treating and polypuroleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, inflammatory conditions such as arthritis, nephritis, Crohn's disease, and is involved in increasing haematopolesis, stem cell survival, bone growth creating transgenic animals useful for cartudying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve carcesthe proliferation of neural cells and regeneration of nerve card, brain tissue and is useful for treatment of central and parkinson's disease, inntington's disease, and amyotrophic lateral cartifity regulation of hematopolesis and is useful for treatment of parkinson's disease, inntington's disease, and amyotrophic lateral spirity regulation of hematopolesis and is useful for treating mysloid of corlymphoid cell disorders, placelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissues repair, healing of burns, inclains, and in tissues proporesis, osteoarthritis, bone degenerative disorders including severe combined immunodeficiency (SCID), bacterial or reperfusion injury in various tissues, various immune deficiencias and disorders and conditions, autoimmune disorders e.g. multiple sclerosis, creations and conditions, autoimmune disorders e.g. multiple sclerosis, creations and conditions, autoimmune disorders e.g. multiple sclerosis, creations and conditions, autoimmune disorders e.g. multiple gravity made disperse mellitus, myasthenia gravis, allergic creations and conditions, autoimmune disorders e.g. multiple gravity made conditions, autoimmune disorders enditions, myasthenia gravia, allergic creations and conditions, autoimmune disorders in multiple gravity and can act as an antigen in a vaccine composition or eliminat
 ö
 modulator; interaction domain; transcription factor; TCF 4; oncogenic; tumor'suppressor gene; conductin; E-cadherin; screening; carcinoma; APC; Wht, signalling.pathway; tumor development; anti-oncogenic; melanoma; organ, regeneration; tissue regeneration; hair growth; mutant.
 Beta-catenin; human; armadillo repeat; treatment; human disease; LEF-1;
 Gaps
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 Length 800;
 Human; beta-catenin.protein mutant armadillo repeat arm 9.
 0; Indels
 1 RHOEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 100.0%; Score 241; DB 22;
arity 100.0%; Pred. No. 1.7e-26;
onservative 0; Mismatches 0;
 Example 2; SEQLIDANO, 663; 107pp; English.
 amino acid sequences of the invention
 AAY33238 standard; peptide; 45 AA.
 99DE-1009251
 (first entry)
 Best Local Similarity 100.
Matches 46; Conservative
 sapiens.
 DE19909251-A1.
 22-FEB-1999;
 18 NOV-1999
 26-AUG-1999.
 Homo sapien
Synthetic.
 Seguence
 AAY33238;
 Query Match
 RESULT., 7
AAY33238
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- 12, 5 - 12, 5

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGICA SABLOGIL), expressed DNA
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
 developmental biology; cell signalling; insecticide;
 ö
 Disclosure; SEQ ID NO 24249; 21pp + Sequence Listing; English
 Disclosure; SEQ ID NO 7380; 21pp + Sequence Listing; English.
 Score 195; DB 22; Length 840;
 Indels
 sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 Drosophila melanogaster polypeptide SEQ ID NO 24249.
 4
 le-19;
 at_ftp.wipo.int/pub/published_pct_sequences.
 Pred. No. le-1
6; Mismatches
 Myers EW;
 Myers EW;
 ABB65819 standard; Protein; 840 AA.
 Li PWD,
 Li PWD,
 :80.98;
 Query: Match 80.9%;
Best Local Similarity 78.3%;
Matches 36; Conservative
 23 - MAR-2001; 2001WO-US09231.
 23 MAR-2000; 2000US-191637P.
11:JUL-2000; 2000US-0614150.
 (first entry)
 Drosophila melanogaster.
(PEKE:) PE CORP NY.
 Adams M,
 Venter JC, Adams M,
 WPI 2001-656860/75.
 WPI: 2001-656860/75
 (PEKE') PE CORP NY.
 N-FSDB; ABL04299
 WO200171042-A2.
 interactions -
 pharmaceutical.
 interactions -
 26-MAR-2002
 Venter JC,
 27-SEP-2001
 Drcsophila;
 Sequence
 ABB65819;
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 ABB65819.
 ŏ
 Op
 This invention describes a novel agent (A) for treating human disease which is based on substances (I) that modulate (inhibit or promote) the interaction of beta-catenin with transcription factors or products of interaction of beta-catenin with transcription factors or products of tumor suppressor genes. The invention also describes (a) peptides (II) comprising part of the LEF-1/TCF4 transcription factors, or their comprising part of the LeF-1/TCF4 transcription factors, or their armadillo domain (arm units 3-8) of beta-catenin, and mutants of the complete beta-catenin molecule, that include at least one of the complete beta-catenin molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or specific interaction domains for LEF-1, TCF-4, APC, conductin or screening substance libraries for compounds that modulate interaction of beta-catenin with LEF-1/TCF, APC, conductin or E-cadherin. Beta-catenin component of tumors. Generally its interaction with LEF-1/TCF, APC, conductin or E-cadherin is a key compound in the Wnt signalling pathway and is involved in development of tumors. Generally its interaction are particularly used to concogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic. (A) which inhibit interaction are particularly used to create they promote interaction, to stimulate regeneration of organs and tissues, specifically mair growth. AAY33230.Y33341 represent mutant the house in the method of the signal of the colon and melanoma.
 ä
 Gaps
 Drosophila; developmental biology; cell signalling; insecticide;
 Agents for treating human diseases, particularly cancer, modular interaction of beta-catenin with transcription factors or tumor
 Score 225.5; DB 20; Length 45;
Pred. No. 9.6e-26;
0; Mismatches 0; Indels 1;
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 Drosophila melanogaster polypeptide SEQ ID NO 7380.
 (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 ABB60196 standard; Protein; 840 AA.
 Example 4; Fig 5; 16pp; German.
 93.6%;
97.8%;
 2000US-191637P
2000US-0614150
 23-MAR-2001; 2001WO-US09231
 Birchmeier W, Von Kries J;
 26-MAR-2002 (first entry)
 suppressor gene products
 Ouery Match 93.6
Best Local Similarity 97.8
Matches 45; Conservative
 Drosophila melanogaster.
 WPI; 1999-470389/40.
 AA;
 WO200171042-A2
 the invention.
 45
 pharmaceutica]
 23-MAR-2000;
11-JUL-2000;
 21-FEB-1998;
 27-SEP-2001.
 ABB60196;
 Sequence
 ABB60196
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δ g ö

Gaps

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The invention is
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30311), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
 at ftp.wipo.int/pub/published_pct_sequences
 840 AA;
 Sequence
×5555555555555×8
```

Gaps ; Indels 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46 4. Score 195; DB 22 Pred. No. 1e-19; 6; Mismatches Query Match 80.9 Best Local Similarity 78.3 Matches 36; Conservative g ò

Drosophila melanogaster polypeptide SEQ ID NO 24255. ABB65821 standard; Protein; 840 AA (first entry) 26-MAR-2002 ABB65821; 10 ABB65821 RESULT 

Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster pharmaceutical

WO200171042-A2

27-SEP-2001

2000US-191637P. 2000US-0614150. (PEKE ) PE CORP NY 23-MAR-2000; 11-JUL-2000;

23-MAR-2001; 2001WO-US09231

Myers EW; Li PWD, Adams M, JC, Venter

WPI; 2001-656860/75. N-PSDB; ABL09924.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Disclosure; SEQ ID NO 24255; 21pp + Sequence Listing; English

isThe invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins sequences (ABL01840 (ABB57737-ABB72072)

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

ö Gaps ; 0 Length 840; 479 rhvdselagñavrlnyglsvivkllhppsrwplikaviglirnlal 524 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46 DB 22; Score 195; DB 2: Pred. No. 1e-19; Mismatches 9 80.9%; Conservative Similarity Local Sim Seguence Query Match Best Loc Matches δ g X S

840 AA;

AAB56810 standard; Protein; 345 AA AAB56810

RESULT 11

AAB56810;

÷

DB 22; Length 840;

80.9%; 78.3%;

(first entry) 13;MAR-2001

Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease. Human prostate cancer antigen protein sequence SEQ ID NO:1388.

Homo sapiens

WO200055174-A1.

21-SEP-2000.

2000WO-US05988 08-MAR-2000; 99US-0124270 L2-MAR-1999;

(HUMA-) HUMAN GENOME (RÔSE/) ROSEN C A.

(ROSE/)

Ruben SM; Rosen, CA, WPI: 2000-587513/55 N-FSDB; AAF16013 Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer

Claim'11; Page 1813-1815; 2338pp; English.

AAFI5566 to AAF16505 encode the human prostate cancer associated profeins, called prostate cancer antigens, given in AAB55363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardiactive; immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaacological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat discretes such as neural, immune, muscular, reproductive discretinal, pulmonary, cardiovascular, renal, and proliferative discretes; wounds, and infectious diseases. AAF16506 to AAF16514 to invention.

345 AA; Seguence

Query Match

Length 345; DB 21; Score 190; 78.88; ö

Gaps

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```
Recombinant tumour PEX protein; phosphate regulating gene; inhibition; endopeptidases; metalloendopeptidase; tumour; OHO; PEX active site; oncogenous hypophosphataemia osteomalacia; chronic renal failure;
 This is the amino acid sequence of the recombinant human tumour PEX protein a product of a phosphate regulating gene with homology to endopeptidases, suggesting that PEX might be a metalloendospetidase. It was isolated from tumours causing oncogenous hypophosphataemia osteomalacia (OHO). Compounds which are targeted to inhibit PEX active site, identified in the method of the invention, are useful for the treatment of hyporphosphataemia or chronic renal failure. PEX can also be used as a target for the treatment of idiopathic
 4; Indels
 DNA encoding human PEX - useful for the treatment of hyper:phosphataemia or chronic renal failure
 Lipman ML;
 DB 19;
11;
 Amino acid sequence of human tumour PEX protein.
 8; Mismatches
 9; Mismatches
 143 mnekaiekadgkpllhilrhspfrwpvlesnig 175
 . MAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVG 39
 Karaplis AC,
 Score 58;
Pred. No.
 Disclosure; Fig 1A-1G; 27pp; English.
 AAW53457 standard; Protein; 749 AA
 24.18;
 97WO-CA00617
 96US-0025454
 Henderson JE,
 (first entry)
 Query Match 24.1
Best Local Similarity 30.3
Matches 10; Conservative
 Matches 34; Conservative
 idiopathic hypercalcuria
 GOLTZMAN D.
HENDERSON J E.
 KARAPLIS A C.
LIPMAN M L.
 WPI; 1998-193628/17.
N-PSDB; AAV23264.
 749 AA;
 Shen Y;
 (LIPM/) LIPMAN M
(PAND/) PANDA D.
(SHEN/) SHEN Y.
 ď
 hypercalcuria.
 Homo sapiens
 WOS810078-A2
 04-SEP-1997;
 05-SEP-1996;
 28-JUL-1998
 12-MAR-1998.
 Goltzman D,
 AAW53457;
 Sequence
 Panda D,
 (COLT/)
 KARA/)
 (HEND/)
 RESULT, 713
 AAW53457
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 X DX DX XX
 δλ
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 Gaps
 in
 The ligand pref. includes a fragment indicated in the features, or the total protein. The ligand pref. contains only a single BS and has an amino acid sequence <100 (pref. <20) residues in length. The ligand may also comprise a plurality of fragment 389..394. A therapeutic compsn. contg. the polypeptide is used to stimulate or inhibit B lymphocyte proliferation in patients with B cell lymphoma. B lymphocytes and myeloma's can be stimulated in patients with immunodeficiencies and immunoglobulin secretion by hybridoma cultures can be boosted. The compsn. can be administered to inhibit infection in vitro or in
 Cellular receptor 2; CR2; binding site; BS; auto-immune disease; Epstein-Barr Virus; EBV; B lymphocyte; ligand.
 ဌ
 ó
 nseq
 4; Indels
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 DNA segment encoding CR-2 ligand and CR2 binding site treat auto-immune disease, B-cell lymphoma and inhibit Epstein-Barr virus infection
 .309
te= "fragment most pref. included"
 /note= "fragment most pref. included"
 Location/Qualifiers
300..312
/note="fragment pref. included"
303..309
 /note= "fragment most pref. inclu
385..400
/note= "fragment pref. inlcuded"
389..394
 Pred. No. 1.8e-19;
 Mismatches
 AAR11354 standard; Protein; 700 AA
 Disclosure; Fig 1; 129pp; English.
 8,
 73.98;
 90WO-US05027,
 90US-0512118.
89US-0404679.
 INST BIOLOGIC
 Epstein-Barr Virus.
 Cellular Receptor 2 ligand.
 03-JUN-1991 (first entry)
Best Local Similarity 73.9
Matches 34; Conservative
 See also AAQ11140-42.
 WPI; 1991-101864/14.
 700 AA;
 N-PSDB; AAQ11140.
 (CALB-) CALIF
 Binding-site
 Binding-site
 Binding-site
 Binding-site
 04-SEP-1990;
 20-APR-1990;
 08-SEP-1989;
 Lernhardt W;
 WO9103251-A
 21-MAR-1991
 Synthetic
 AAR11354;
 Sequence
 vivo by
 NAME OF THE PROPERTY OF THE PR
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ö Gaps ; Length 749; 14; Indels RESULT

Length 700;

Score 190; DB 12; Pred. No. 4.3e-19;

78.8%; 73.9%;

Query Match Best Local Similarity

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABD101840-ABL16175) and the encoded proteins refraction; but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
 Disclosure; SEQ ID NO 678; 21pp + Sequence Listing; English.
 141 aqyaapav-ahyaapavvktvapvahyaapavvktvapvahya 182
 DB 22;
 1.5 AEMAQNAVRLHYGLPVVVKLLHPPSHW--PLIKATVGLIRNLA
 23.9%; Score 57.5; E 37.2%; Pred. No. 2.9;
 7; Mismatches
 Myers EW;
 completed: July 29, 2002, 16:07:58 e: 648 sec
 Venter JC, Adams M, 'Li PWD,
 23 MAR-2001; 2001WO-US09231.
 23 MAR-2000; 2000US-191637P.
 2000US-0614150
 New isolated nucleic acid
genes! from Drosophila and
interactions -
 Query:Match
Best Local Similarity 37.2
Matches 16; Conservative
Drösöphila melänogaster.
 WPI: 2001-656860/75.
 (PEKE") PE CORP NY.
 221 AA;
 N-PSDB; ABL02065
 W6200171042-A2
 ESEP-2001.
 11-JUL-2000;
 Seguence
 Search,
 g
 ŏ
 ä
 13
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
 Gaps
 developmental biology; cell signalling; insecticide;
 3;
 Length 205;
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 Indels
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 Score 57.5; DB 22;
Pred. No. 2.7;
 ftp.wipo.int/pub/published_pct_sequences.
 7; Mismatches
 Myers EW;
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 PWD,
 23.9%;
 23-MAR-2001; 2001WO-US09231
 2000US-191637P
 2000US-0614150
 (first entry)
 Conservative
 Ħ
 Drosophila melanogaster
 Venter JC, Adams M,
 WPI; 2001-656860/75
 ABB57737-ABB72072)
 Query Match
Best Local Similarity
Matches 16; Conserv
 (PEKE) PE CORP NY
 205 AA;
 N-PSDB; ABL03144
 WO200171042-A2
 pharmaceutical
 11-JUL-2000;
 interactions
 23-MAR-2000;
 26-MAR-2002
 Drosophila;
 Sequence
 ABB59041;
 ABB59041
 NAMES OF COLOR OF STREET O
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Gaps

ë

Indels

Drosophila; developmental biology; cell signalling; insecticide;

pharmaceutical.

Drosophila melanogaster polypeptide SEQ ID NO 678

26-MAR-2002 (first entry)

ABB57962;

AA

ABB57962 standard; Protein; 221

15

ABB57962

Length 221;

(OTASU) MANALO 30A9 SIHT

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 29, 2002, 16:05:12; Search time 57.6 Seconds Run on:

(without alignments)
19.507 Million cell updates/sec

US-09-641-104A-12

241 1 RHQEAEMAQNAVRLHYGLPV......PPSHWPLIKATVGLIRNLAL

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

231628 seqs, 24425594 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
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5: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | æ     |        |    | SUMMARIES         |                   |
|---------------|-------|-------|--------|----|-------------------|-------------------|
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| 7             | 54.5  | 22.6  | 416    | 4  | US-09-333-254-2   | 7                 |
| e             | 54    | 22.4  | 885    | ~  | US-08-500-857A-8  | æ                 |
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| 12            | 51    | 21.2  |        | m  | US-08-941-936-2   | 2, 4              |
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TYPE: PRT ORGANISM: Pseudomonas mendocina KR-1

|      | Sequence 5, Appli | Sequence 5, Appli | Seguence 2, Appli | Sequence 1, Appli           | Sequence 25, Appl | Sequence 38, Appl | Sequence 23, Appl | Seguence 23, Appl | Sequence 23, Appl | Sequence 9, Appli | Sequence 13, Appl | Sequence 4, Appli | Sequence 25, Appl | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 48, Appl |      |
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| - 1. | ·                 | <br>G             |                   | ); (*)<br>(*)<br>(*)<br>(*) |                   | 3                 |                   |                   | ; ,               |                   | · ·               | 6                 |                   | . ,<br>           | 2                 | 3, 1.             | -                 | ٠.                | ٠. ; |
|      | 28                | 2                 | 3(                | 3,                          | 'n                | 'n                | 34                | 3,5               | 36                | 'n                | 3                 | ,<br>ω            | 4                 | 4                 | 4                 | 4                 | 4                 | 4                 |      |

## ALIGNMENTS

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 APPLICANT: Chen K.
TITLE OF INVENTION: A Gene Encoding a Putative Efflux Protein for Solvents/
TITLE OF INVENTION: Antibiotics in Pseudomonas Mendocina
FILE REPRENCE: CL-1160-D
CURRENT APPLICATION NUMBER: US/09/333,254A
CURRENT FILING DATE: 1999-06-15
EARLIER PLING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Microsoft.Office 97
 Gaps
 GENERAL INFOGRATION:

PAPLICANT: Chen, Kevin K.

TITLE OF INVENTION: A Putative Solvent/Antibiotic Resistant Gene from TITLE OF INVENTION: Pseudomonas Mendocina FILE, REFERENCE: CL-1160-C CURRENT APPLICATION NUMBER: US/09/33,208A CURRENT FILING DATE: 1999-06-15 EARLIER APPLICATION NUMBER: 09/183,270 EARLIER PILING DATE: 1998-10-30 NUMBER OF SEQ ID NOS: 6
SOFTWARE: Microsoft Office 97
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LENGTH: 416
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 11 AVRLHYGLPVVVKLL -- HPPSHWPLIKATV 38
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US-09-333-208-2
 Sequence 2. Application US/09333254A
; Patent No. 6235882
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 Sequence 2, Application US/0933208A Patent No. 6225089 GENERAL INFORMATION:
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LENGTH: 416
RESULT 1,
US-09-333-208-2
 US-09-333-254-2
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3:28:

δ pp

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4;
 GENERAL INFORMATION:..
APPLICANT: Takashi OKADO et al.
TITLE OF INVENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY
NUMBER OF SEQUENCE: 50
CORRESPONDENCE: ADDRESS:
 DB 4; Length 439;
 Indels
 2; Mismatches 16;
 192 HYGAPFVCSLIMFIFGPPGTVPLFARTFGYISMTAV 227
 15 HYGLPVVVKLL----HPPSHWPLIKATVGLIRNLAL 46
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Pifteenth Street, N.W., #700
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb.
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
 STREET: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
 STATE: D.C.
COUMTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE:FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM COMPATIBLE
 Score 53;
Pred. No.
 APPLICATION NUMBER: US/08/716,873
FILING DATE: September 20, 1996
 APPLICATION NUMBER: US/08/716, FILING DATE: September 20, 199
 US-08-716-873-4; Sequence 4, Application US/08716873; Patent No. 6194166
 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
 22.0%;
38.9%;
 OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION:DATA:
 را
.:
 ATTORNEY/AGENT INFORMATION:
 : 439 amino acids
amino acid
 REFERENCE/DOCKET NUMBER
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 Query Match 22.0
Best Local Similarity 38.9
Matches 14; Conservative
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
 single
 ; MOLECULE TYPE: peptide US-08-716-873-2
 CLASSIFICATION: 435
PRIOR-APPLICATION DATA:
APPLICATION NUMBER:
 CITY: Washington STATE: D.C
 COUNTRY: U.S.A.
 linear
 FILING DATE: Se
CLASSIFICATION:
 STRANDEDNESS:
 FILING DATE:
 LENGTH:
 В
 ò
 Sequence 8, Application US/08500857A

Patent No. 5912156

GENERAL INFORMATION:
APPLICANT: OHATA, SHOZO
APPLICANT: OHATA, SHOZO
APPLICANT: OHATA, SHOZO
APPLICANT: OHATA, SHOZO
APPLICANT: OF INVENTION: POLYPEPTIDE HAVING COLD-STABLE PYRUVATE,
TITLE OF INVENTION: ORTHOPHOSPHATE DIKINASE ACTIVITY, DNA ENCODING THE SAME
TITLE OF INVENTION: THE DNA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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 Gaps
 3;
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0
 Sequence 2, Application US/08716873
Patent No. 6194166
GENERAL INFORMATION:
APPLICANT: TARASHI OKADO et al.
TITLE OF INVENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY
 Score 54.5; DB 4; Length 416; Pred. No. 3.9;
 Score 54; DB 2; Length 885; Pred. No. 12;
 Indels
 Indels
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: 8110 GATE HOUSE ROAD SUITE 500 EAST
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,857A
 12;
 4; Mismatches
 1; Mismatches
 344 AMYLVYGCVVTAALIFVVQPSGHWPLVAAVL 374
 11 AVRLHYGLPVVVKLL---HPPSHWPLIKATV 38
 ATTORNEY AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFENCE/DOCKET NUMBER: 760-208P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 103-205-8050
 22.6%;
38.7%;
 : 885 amino acids
amino acid
 Query Match
Best Local Similarity 38.73
Matches 12; Conservative
 INFORMATION FOR SEQ ID NO:
 Query Match
Best Local Similarity 71.4
Matches 10; Conservative
 SEQUENCE CHARACTERISTICS
 protein
 ||||| |:|| || |
611 GLPVTVRLLDPPLH 624
 FILING DATE:
CLASSIFICATION: 435
 17 GLPVVVKLLHPPSH 30
 STREET: 8110 GATE I
CITY: FALLS CHURCH
STATE: VA
 USA
 ; MOLECULE TYPE:
US-08-500-857A-8
 22042
 TOPOLOGY:
 RESULT 3
US-08-500-857A-8
 COUNTRY:
US-09-333-254-2
 US-08-716-873-2
 LENGTH:
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Gaps

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 4,
 APFLICANT: TAKASHI OKADO et al.
TITLE OF INVENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY
TITLE OF INVENTION: (AS AMENDED)
UNUMBER OF SEQUENCES: 50
COKRESPONDENCE ADDRESS:
 22.0%; Score 53; DB 4; Length 439; 38.9%; Pred. No. 7;
 DB 4; Length 439;
 Score 53; DB 4; Length 439
Pred. No. 7;
2; Mismatches 16; Indels
 Indels
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 192 HYGAPFVCSLIMFIFGPPGTVPLFARTFGYISMTAV 227
 , 15 HYGLPVVVKLL----HPPSHWPLIKATVGLIRNLAL 46
 15 HYGLPVVVKLL----HPPSHWPLIKATVGLIRNLAL 46
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: AUGUST 5, 1999
 2; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/716,873
FILING DATE: September 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: 202-721-8200
TELEFRAX: 202-721-8250
 August 5, 1999
 Sequence 2, Application US/08500857A Patent No. 5912156 GENERAL INFORMATION:
 Sequence 4, Application US/09368431
Patent No. 6294651
GENERAL INFORMATION:
 USAMI, STORU
BURNELL, JAMES N
 22.0%;
38.9%;
 439 amino acids
 Best_Eocal Similarity 38.9
Matches 14; Conservative
 Ouery Match 22.0 Best Local Similarity 38.9 Matches 14; Conservative
 SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO:
 OHATA, SHOZO
 ; MOLECULE TYPE: peptide US-09-368-431-4
 amino acid
 linear
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 CLASSIFICATION:
 STRANDEDNESS:
 CITY: Wash:
STATE: D.C.
 IOPOLOGY:
 RESULT : 8
US-08-500-857A-2
 APPLICANT:
APPLICANT:
 RESULT 7
US-09-368-431-4
 APPLICANT:
 Query Match
 Qγ
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 Dp
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 4;
 GENERAL INFORMATION:
APPLICANT: Takashi OKADO et al.
TITLE OF INVENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY
TITLE OF INVENTION: (AS AMENDED)
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
 DB 4; Length 439;
 Indels
 16;
 ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P. STREET: 2033 K Street, N.W., #800
 192 HYGAPFVCSLIMFIFGPPGTVPLFARTFGYISMTAV 227
 15 HYGLPVVVKLL----HPPSHWPLIKATVGLIRNLAL 46
 2; Mismatches
 COUNTRY: U.S.A.
21P: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 Score 53;
Pred. No.
 UMBER: US/09/368,431
August 5, 1999
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/716,873
FILING DATE: September 20, 1996
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION UNUMBER: 33,367
REFERENCE/CDCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
 78-09-368-431-2
; Sequence 2, Application US/09368431
; Patent No. 6294651
 NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
 CURENT APPLICATION DATA:

APPLICATION NUMBER: US/09/36
FILING DATE: AUGUST
CLASSIPTT
 Query Match 22.0%;
Best Local Similarity 38.9%;
Matches 14; Conservative
 COMPUTER: IBM Compatible
 LENGTH: 439 amino acids
 SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 SS: single
linear
 INFORMATION FOR SEQ ID NO:
 ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-716-873-4
 TYPE: amino acid
STRANDEDNESS: single
 TYPE: amino acid
STRANDEDNESS: sin
 CITY: Washington
 linear
 TOPOLOGY: 11
MOLECULE TYPE:
 D.C.
 TELEFAX:
 US-09-368-431-2
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 Gaps
 Gaps
 APPLICANT:
TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING
 TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR NUMBER OF SEQUENCES: 27
 ;
0
 ;
0
 Length 649;
 Length 955;
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/300,909
 Score 51; DB 4;
Pred. No. 22;
4; Mismatches
 Score 53; DB 2;
Pred. No. 18;
2; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/083,942
FILING DATE:: 01-MAY-1998
INFORMATION FOR SEC ID NO: 15:
SEQUENCE CHARACTERISTICS:
 PC-DOS/MS-DOS
 ; Sequence'15, Application US/09300909; Patent No. 6306580; GENERAL INFORMATION:
 176. HTEAEAPTNSVREHAGTAGILELL 199
 ; Sequence 27, Application US/09300909; Patent No. 6306580
 1..2 HQEAEMAQNAVRLHYGLPVVVKLL 25
 REFERENCE/DOCKET NUMBER: 760-
TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8050
TELEPRAX: 103-205-8050
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 955 amino acids
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
EILING DATE: 435
CLASSIFICATION: 435
ATTORNEY AGENT-INFORMATION:
NAME: MURPHY JR; GERALD M
REGISTRATION NUMBER: 28,977
 28,977
 22.0%;
 Ouery Match
Best Local Similarity ,45.8%;
Matches 11; Conservative
 NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE:: Floppy disk
 Query Match
Best Local Similarity 64.3v,
Best Local Similarity 64.3v,
 LENGTH: 649 amino acids
 MOLECULE TYPE: protein US-08-500-857A-10
 MOLECULE TYPE: protein
 ||||| ::|| || |
| 694 GLPVTIRLLDPPLH 707
 17 GLPVVVKLLHPPSH 30
 amino acid
 ropology: linear
 GENERAL, INFORMATION:
 STRANDEDNESS:
 FILING DATE:
 RESULT '10,
US-09-300-909-15
 US-09-300-909-15
 US-09-300-909-27
 RESULT 11
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 g
 APPLICANT: USAMI, SHOZO
APPLICANT: USAMI, STORU
APPLICANT: USAMI, STORU
APPLICANT: USAMI, STORU
APPLICANT: BURNELL, JAMES N
TITLE OF INVENTION: POLYPEPPIDE HAVING COLD-STABLE PYRUVATE,
TITLE OF INVENTION: ORTHOPHOSPHATE DIKINASE ACTIVITY, DNA ENCODING THE SAME
TITLE OF INVENTION: THE DNA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: 8110 GATE HOUSE ROAD SUITE 500 EAST
 ORTHOPHOSPHATE DIKINASE ACTIVITY, DNA ENCODING THE SAME AND RECOMBINANT VECTOR AND TRANSFORMED PLANTS CONTAINING THE DNA
 ö
 ö
 POLYPEPTIDE HAVING COLD-STABLE PYRUVATE,
 DB 2; Length 953;
18;
 Indels
 NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: 8110 GATE HOUSE ROAD SUITE 500 EAST
CITY: FALLS CHURCH
 ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/500,857A
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/500,857A
 Mismatches
 Score 53;
Pred. No.
 US-08-500-857A-10
; Sequence 10, Application US/08500857A
; Patent No. 5912156
; GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 CLASSIFICATION: 435
ATTORNEY/AGENY INFORMATION:
NAME: MURRHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
 TELEFAX: 103-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 953 aniho acids
TYPE: amino acids
 22.0%;
64.3%;
 Query Match 22.0
Best Local Similarity 64.3
Matches 9; Conservative
 MOLECULE TYPE: protein
 (111 ::11 || |
692 GLPVTIRLLDPPLH 705
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 17 GLPVVVKLLHPPSH 30
 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
 FALLS CHURCH
 USA
 FILING DATE:
 22042
 Κ
 Ϋ́
 US-08-500-857A-2
 COUNTRY:
 COUNTRY:
 CITY: F
 STATE:
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us-09-641-104a-12.rai

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 Gaps
 APPLICANT: FORG JOHN
APPLICANT: FORG JOHN
APPLICANT: FORG JOHN
APPLICANT: WILLEON JULIO
APPLICANT: WILLEON JULIO
APPLICANT: WEUNG, GEORGE
TITLE: OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE: OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE: OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE: REPERENCE: 28110/36570
CURRENT APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-01-16
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 09/118,205
 11;
 ;
0
 METHODS AND MATERIALS RELATING TO CD39-LIKE
 Score 49.5; DB 4; Length 405;
Pred. No. 21;
2; Mismatches 12; Indels 1.
 Score 51; DB 3; Length 878;
Pred. No. 32;
 99 QGAETVQ-----GLLEVAKDSIPRSHWKKTPVVLKATAGL 133
 3 QEAEMAQNAVRLHYGLPVVVKLLHPPSHWP----LIKATVGL 40
 3; Mismatches
 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR FILING DATE: 1998-07-16 NUMBER OF SEQ ID NOS: 60
 Sequence 25, Application US/09608285A Patent No. 6335013
 US-09-608-285A-3
; Sequence 3, Application US/09608285A
; Patent No. 6335013
 Query Match 20.5%;
Best Local Similarity 40.5%;
Matches 17; Conservative
 Query Match
Best Local Similarity 57.1
Matches 8; Conservative
 GENERAL INFORMATION:
APPLICANT: FOTG, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHO
 617 GLPVTIRLIDPPLH 630
 17 GLPVVVKLLHPPSH 30
 TYPE: PRT
ORGANISM: Homo sapiens
 MOLECULE TYPE:
 RESULT 13
US-09-608-285A-25
 US-09-608-285A-25
 ; MULECULE 11
US-08-941-936-2
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 q
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 g
 Pyruvate Orthophosphate Dikinase Gene,
Recombinant DNA, and Process For Producing Pyruvate
Orthophosphate Dikinase
 ö
TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM: 27
COMPUTER: IDAM PYPE: FLOAPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,909
FILING DATE: 01-MAY-1998
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
 Length 649;
 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
 Score 51; DB 4;
Pred. No. 22;
 STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
 Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HIRAKI-03009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-705-8410
 APPLICATION NUMBER: US/08/941,936
FILING DATE: 01-OCT-1997
CLASSIFICATION: 435
 MEDLEN & CARROLL, LLP
 2 HQEAEMAQNAVRLHYGLPVVVKLL 25
 Sequence 2, Application US/08941936
Patent No. 6054305
 4;
 GENERAL INFORMATION:
APPLICANT: Tatsumi, Hiroki
APPLICANT: Tatsumi, Hiroki
APPLICANT: Bisaki, Naoki
APPLICANT: Horiuchi, Tatsuo
APPLICANT: Nagahara, Ayumu
TITLE OF INVENTION: Recombinan
TITLE OF INVENTION: Orthophosp
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
 E: Floppy disk
IBM PC compatible
 Query Match 21.2%;
Best Local Similarity 45.8%;
Matches 11; Conservative 4
 TELEFAX: 415-397-8338 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 649 amino acids TYPE: amino acid
 SEQUENCE CHARACTERISTICS:
LENGTH: 878 amino acid
TYPE: amino acid
 CURRENT APPLICATION DATA:
 415-397-8338
 single
 : MOLECULE TYPE: protein US-09-300-909-27
 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 OPERATING SYSTEM:
SOFTWARE: PatentI
 linear
 TOPOLOGY: linear
 STRANDEDNESS:
 S
 ADDRESSEE:
 COMPUTER:
 COUNTRY:
 US-08-941-936-2
 STATE:
```

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Gaps
 Score 49.5; DB 4; Length 428;
Pred. No. 23;
2; Mismatches 12; Indels 11;
 DB 4; Length 428;
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 3 QEAEMAQNAVRLHYGLPVVVKLLHPPSHWP----LIKATVGL 40
 Search completed: July 29, 2002, 16:05:13
Job time: 483 sec
 20.5%;
 1998-07-16
 PatentIn Ver. 2.0
 17; Conservative
PRIOR, APPLICATION NUMBER:
PRIOR, FILING DATE: 1998-07
 ORGANISM: Homo sapiens
 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 5
LENGTH: 428
 Query Match
Best Local Similarity
Matches 17; Conserv
 US-09-608-285A-5
 TYPE: PRT
 ōλ
 qq
 ;
;
 Gaps
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE TITLE OF INVENTION: POLYPEPTIDES FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: __09/583,231
 11;
 Score 49.5; DB 4; Length 428;
Pred. No. 23;
 2; Mismatches 12; Indels
 99 QGAETVQ-----GLLEVAKDSIPRSHWKKTPVVLKATAGL 133
 3 QEAEMAQNAVRLHYGLPVVVKLLHPPSHWP----LIKATVGL 40
 US/09/608,285A
 PCT/US99/16180
 J999-07-16
 PRIOR APPLICATION NUMBER: 09/557,800
PRIOR PILING DATE: 2000-04-25
PRIOR PLILNG DATE: 2000-04-25
PRIOR FILING DATE: 09/370,265
PRIOR FILING DATE: 1099-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR PLING DATE: 1999-07-16
PRIOR PLING DATE: 1999-07-09
PRIOR PLILNG DATE: 1999-07-09
PRIOR PLILNG DATE: 1999-07-09
PRIOR PLILNG DATE: 1999-07-09
 CURRENT FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PLICATION NUMBER: 09/583,231
PRIOR PELICATION NUMBER: 09/557,800
PRIOR PELICATION NUMBER: 09/370,255
PRIOR PELICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR PLICATION NUMBER: 09/370,265
PRIOR PLICATION NUMBER: 09/370,365
PRIOR PLICATION NUMBER: 09/370,347
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR PLING DATE: 1999-03-04
PRIOR PLING DATE: 1998-07-24
 MBER: 09/122,449
1998-07-24
 09/244,444
 Sequence 5, Application US/09608285A Patent No. 6335013 GENERAL INFORMATION:
 POLYPEPTIDES
 2000-05-26
 999-02-04
 Query Match 20.5%;
Best Local Similarity 40.5%;
Matches 17; Conservative
 PRIOR APPLICATION NUMBER: 09, PRIOR FILING DATE: 1998-07-1 NUMBER OF SEQ ID NOS: 60 SOFTWARE: PAtentin Ver. 2.0 SEQ ID NO 3
 Mulero, Julio
Yeung, George
 ; ORGANISM: Homo sapiens US-09-608-285A-3
 PRIOR FILING DATE:
 ·09-608-285A-5
 LENGTH:
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 29, 2002, 16:09:17; Search time 70.63 Seconds (without alignments) 62.581 Million cell updates/sec

US-09-641-104A-12 Title:

241 1 RHQEAEMAQNAVKLHYGLPV......PPSHWPLIKATVGLIRNLAL Perfect score:

Sequence:

283138 seqs, 96089334 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*

Database

pir1:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | d              |        |    | SUMMARIES |                     |
|---------------|-------|----------------|--------|----|-----------|---------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB | ID        | Description         |
| П             | 241   | 100.0          | 781    | 2  | 835099    | beta-catenin - Afr  |
| 7             | 241   | 100.0          | 781    | 7  | A38973    | beta-catenin - hum  |
| ю             | ,241  | 100.0          | 781    | 7  | ന         | beta-catenin - mou  |
| 4             | 218   | 90.5           | 817    | 7  | S33793    | hypothetical prote  |
| S             | 202   | 83.8           | 820    | 7  | S33794    | hypothetical prote  |
| 9             | 201   | 83.4           | 738    | ~  | S35093    | plakoglobin - Afri  |
| 7             | 195   | 80.9           | 843    | 7  | T12689    | armadillo segment   |
| 80            | 190   | 78.8           | 621    | 7  | S35092    | plakoglobin - mous  |
| 6             | 190.  | 78.8           |        | 7  | A32905    | plakoglobin, desmo  |
| 10            | 188   | 78.0           |        | 7  | JC4835    | c                   |
| 11            | 78.5  | 32.6           |        | ~  | T23341    | •                   |
| 12            | 63.5  | 26.3           | 1050   | 7  | T26395    | hypothetical prote  |
| 13            | 59.5  | 24.7           | 351    | 7  | F90409    | O                   |
| 14            | 58.5  | 24.3           | 578    | 7  | S50446    | VAC8 protein - yea  |
| 15            | 56.5  | 23.4           | 393    | 1  | E64485    | phosphoribosylglyc  |
| 16            | 56.5  | 23.4           | 555    | 7  | T40294    | hypothetical prote  |
| 17            | . 56  | 23.2           | 806    | 7  | AE2675    | pyruvate, orthophos |
| 18            | 26    | 23.2           | 933    | 7  | C97457    | pyruvate, phosphat  |
| 19            | 55.5  | 23.0           | 160    | 7  | S26194    | plastoquinolplas    |
| 20            | 55    | 22.8           | 224    | 7  | н82658    | carboxylesterase X  |
| 21            | 52    | 22.8           | 441    | 7  | A84351    | hypothetical prote  |
| 22            | 52    | 22.8           | 503    | 7  | G81917    | σ                   |
| 23            | 52    | 22.8           | 842    | 7  | T23715    | hypothetical prote  |
| 24            | 52    | 22.8           | 1160   | 7  | T23713    |                     |
| 25            | 52    | 22.8           | 1286   | 7  | T23714    | _                   |
| 26            | 54    | 22.4           | 885    | 7  | S36601    | ᅩ                   |
| 27            | 54    | 22.4           | 1094   | 7  | T00814    | RNA-directed DNA p  |
| 28            | 54    | 22.4           | 1124   | N  | S23820    | pol polyprotein -   |
| 29            | 53.5  | 22.2           | 396    | 7  | D82394    | GGDEF family prote  |

| probable coiled co | probable olfactory | cell cycle protein | ubiquinone biosynt | pyruvate, orthophos | pyruvate, orthophos | pyruvate phosphate | pyruvate phosphate | pyruvate, phosphat | pyruvate, orthophos | pyruvate,orthophos | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S62428             | S58075             | B82778             | B81184             | F72397              | T31131              | T37037             | G87431             | AF3431             | T02979              | S55478              | S12894              | S56650              | S56649              | S53297              | A71420             |
| 7                  | ~                  | ~                  | 7                  | ~                   | 7                   | ~                  | 7                  | ~                  | ~                   | Н                   | 7                   | 7                   | 7                   | ~                   | 7                  |
| 899                | 154                | . 437              | 503                | 881                 | 888                 | 868                | 006.               | 930                | 947                 | 949                 | . 953               | 953                 | 955                 | 926                 | 096                |
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| 30                 | 31                 | 32                 | 33                 | 34                  | 35                  | 36                 | 37                 | 38                 | 39                  | 40                  | 41                  | 42                  | 43                  | 44                  | 45                 |

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 Gaps
 ;
0
 Length 781;
 Indels
 ilarity 100.0%; Score 241; DB 2; 100.0%; Pred. No. 7.5e-24; Conservative 0; Mismatches 0;
 Query Match
Best Local Similarity
Matches 46; Conserv
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1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46

474 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 519 qq ŏ

RESULT : 2

A38973 beta-catenin - human

C; Species: How supplens (man),
C; Species: How supplens (man),
C; Species: How supplens (man),
C; Date: 26-Jan-1996 #sequence\_revision 08-Feb-1996 #text\_change 08-Oct-1999
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C; Date: 26-Jan-1996 #sequence\_revision 08-Feb-1996 #text\_change 08-Oct-1999
C; Date: 26-Jan-1996 #sequence ro.
J; Birchmeier; W; Behrens, J.
J; Birchmeier; W; Behrens, J.
J; Birchmeier and APC compete for the interaction with beta-catenin and the cyt
A; Title: E-cadherin and APC compete for the interaction with beta-catenin and the cyt
A; Reference number: A38973
A; Recession: caid sequence not shown
A; Residues: 1-781 'AHUE>
A; Residues: 1-781 'AHUE>
A; Cross-references: GB:219054; NID:338519; PIDN:CAA79497.1; PID:938520
A; Cross-references: GB:219054; NID:938519; PIDN:CAA79497.1; PID:9860988
A; Cross-references: bacearin mRNA
A; Reference number: S55356
A; Accession: S55356
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-781 'ANOLS
A; Cross-references: EMBL:X87838; NID:91154853; PIDN:CAA61107.1; PID:9860988
C; Comment: The cytoplasmic protein beta-catenin normally binds to a region in the cyt

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781;

0; Indels Length

; Score 241; DB 2; ; Pred. No. 7.5e-24; 0; Mismatches 0;

100.0%; 100.0%;

Query Match
Best Local Similarity 100.
Matches 46; Conservative

474 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 519

RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46

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lcrofilament network. Comment: Cellular levels of beta-catenin are regulated in part

microfilament network.
C;Comment: Cellular levels of beta-catenin are regulated in pa d cancerous cell growth.
C;Genetics:
A;Gene : GDB:CTNNB1; CTNNB
A;Cross-references: GDB:141922; OMIM:116806
A;Ross-references: GDB:141922; OMIM:116806
A;Map position: 3p22-3p21.3
C;Keywords: apoptosis; carcinogenesis; cell adhesion; cytosol F;151-676/Region: 40-residue repeats

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 hypothedical protein - sea urchin (Tripneustes gratilla)
C; Species: Tripneustes gratilla
C; Species: Tripneustes gratilla
C; Species: S33794; Sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C; Accession: S33794; Sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C; Accession: S33794; Sequence_revision 1993
A; Tritle: Inchinication of homologues to beta-catenin/plakoglobin/armadillo in two A; Reference number: S33793; MuID: 93305730
A; Accession: S33794; Sequence_revision S43794; S43794
 ö
 ö
 Nalternate names: protein 8684.6
C;Species: Drosophila.melanogaster
C;Date:.13-aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Accession: T12689; A1861
R;Ferraz, C;; Vidal, S;; Brun, C;; Bucheton, A;; Demaille, J.G.
submitted to the EMBL Data Library, January 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17572
A;Accession: T12689;
 plakoglobin - African clawed frog
plakoglobin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: 835093; 824636
R:Fouquet, B.; Zimbelmann, R.; Franke, W.W.
Differentiation 51, 187-194, 1992
A:Title: Identification of plakoglobin in oocytes and early embryos of Xenopoly A:Reference number: 835093; MUID:93093332
 A)Cross-references: EMBL;M95593; NID:g214656; PIDN:AAA49931.1; PID:g214657 R; Demarais, A.A. Submitted to the EMBL Data Library, June 1992 A; Reference number: S24636 A; Accession: S24636
 Gaps
 Gaps
 armadillo segment polarity protein - fruit fly (Drosophila melanogaster)
 .;
0
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0
 Length 738;
 Length 820;
 ;; DB 2; ...
1.2e-18;
5; Indels
 Indels
 461 RHQDAEVAQNSVRLHYGIPAIVKLLNPPYQWPLVKATIGLIRNLAL 506
 1. RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 11' RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 A;Status: preliminary
A;Moleotule,type: mRNA
A;Residues: 133-184, VV,186-225, Tr,227-292 <DEM>
A;Residues: EMBL:X67078; NID:965252; PID:965253
 Score 201; DB 2; L
Pred. No. 1.4e-18;
3; Mismatches 3;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule;type: DNA
 Query, Match 83.4%; Score 201; DB Best Load Similarity 76.1%; Pred. No. 1.4e Matchest, 35; Conservative 8; Mismatches
 Mismatches
 Score 202;
Pred. No. 1
 3;
 cuery Match 83.8%;
Best Local Similarity 82.6%;
Matches 38; Conservative
•
 A; Accession: 533,74;
A; Astatus: preliminary
A; Molecule; type: mRNA
A; Residues: 1-820 <ROS;...
 C; Keywords: cytoskeleton
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-738 <FOU>
 figal protein
 RESULT
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 QQ
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 hypothetical protein - spoonworm (Urechis caupo)
hypothetical protein - spoonworm (Urechis caupo)

S. Specias: Urechis caupo
C. Specias: Urechis caupo
C. Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C. Accession: S33793 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C. Accession: S33793 #sequence_revision 1993
A. Title: Identification of homologues to beta-catenin/plakoglobin/armadillo in two inver A. Reference number: S33793; MUID:93305730
A. Status: preliminary
A. Molecule type: mRNA
A. Molecule type: mRNA
 the adenomatous poly
 Deta-catenin - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mos-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S35091
R;Butz, S; Stappert, J; Weissig, H; Kemler, R.
Science 257, 1142-1144, 1992
A;Title: Plakoglobin and beta-catenin: distinct but closely related.
A;Reference number: S35091; MUID:92376536
A;Reference number: S35091; MUID:92376536
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-781 <BUT>
A;Cross-references: EMBL:M90364; NID:g192141; PIDN:AAA37280.1; PID:g192142
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781;

Length

Indels

474 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 519

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1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46

Query Match 100.0%; Score 241; DB 2; Best Local Similarity 100.0%; Pred. No. 7.5e-24; Matches 46; Conservative 0; Mismatches 0;

RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46 q ò

Length 817;

Score 218; DB 2; Pred. No. 9e-21; Mismatches

1;

Query Match 90.5%; Best Local Similarity 91.3%; Matches 42; Conservative

Molecule type: mRNA Residues: 1-817 <ROS>

RESULT

496

us-09-641-104a-12.rpr

A; Residues: 1-843 <FER>

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Gaps

; 0

Indels

Length 744;

position: 7pter-7gter

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C.Speciges: Caenorhabolits elegans
R.Harris, B.
Submitted to the EMBL Data Library, November 1996
A.Rocession: T23341
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: Land, W.: Agbunag, C.; Hardin, J.; Priess, J.R.
R.Scosti M.: Raich, W.: Agbunag, C.; Hardin, J.; Priess, J.R.
R.Reference number: Z22085
A.Recession: T4221
A.Molecule. Type: mRNA
 Cydrocession: JC4835.
R:Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T. (Chen 17, 155-159, 1996)
R:Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T. (Chen 17, 155-159, 1996)
R:Hobmayer, E.; Hatta, M.; Fischer, R.; Fujisawa, T.; Holstein, T.W.; Sugiyama, T. (Chen 17, 155-159, 1996)
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R; Reference number: JC4835
R; Reference number: JC4835
R; Reference number: JC4835
R; Restauce: JC4835
R; Richard number: JC4
 C;Species: Hydra magnipāpillata
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000
 533 RHPDAEHAENGVRLHYGIPILVKLLNPPSRWPLIKAVVGLIRNLGL 578
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
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 Score 188; DB 2; L
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6; Mismatches 6;
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Pred. No. 4.2e-17;
8; Mismatches 4;
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 A, Map position: 1
A; Introns: '14/1; 235/1; 290/1; 620/3
 beta-catenin - Hydra magnipapillata
 78.8%;
73.9%;
 78.0%;
 Ouery Match
Best Local Similarity 73.9
Matches 34; Conservative
 Matches 34; Conservative
 A; Gene: hmp-2; CESP: K05C4:6
A;Map position: /prer-/y
C;Keywords: cytoskeleton
 Best Local Similarity
 A; Gene: betactn
 Query Match
 Query Match
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 an
 Diakoglobin, desmosomal - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22 Nov-1989 #sequence_revision 22-Nov-1989 #text_change 29-Aug-1997
C;Accession: A31305
R;Franke, W.W.; Goldschmidt, M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cowin,
Proc. Natl. Acad. Sci. U.S.A. 86, 4027-4031, 1989
A;Title: Nolecular cloning and amino acid sequence of human plakoglobin, the common jund
A;Reference number: A32905; MUID:89264555
 A.Cross-references: EMBL: AL021106; NID:e1371406; PID:e1249776; PIDN:CAA15946.1
A.Experimental source: clone cosmid 63B12
A.Experimental source: clone cosmid 63B12
B.Fistgleman, B.; Waschaus, E.; Schedl, P.
Genes Dev. 3, 96-113, 1989
A.Fitle: Molecular analysis of the Armadillo locus: uniformly distributed transcripts A.F. Reference number: A31861; MUID:89211895
A.F. Molecule type: DNA
A.Residues: 1-843 < RIG>
A.R. Molecule type: DNA
A.R. Residues: 1-843 < RIG>
A.Cross-references: EMBL:X54468; NID:97610; PIDN:CAA38350.1; PID:g7611
C.Genetics:
A.Gene: arm
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 Diakoglobin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S35092
R;Butz, S.; Stappert, J.; Weisslg, H.; Kemler, R.
Science 257, 1142-1144, 1992
A;Title: Plakoglobin and beta-catenin: distinct but closely related.
A;Reference number: S35091; MUID:92376536
A;Accession: S35092
A;Accession: S35092
A;Accession: 1621 *CBUT>
A;Molecule type: mRNA
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C;Keywords: cytoskeleton
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0
 Score 190; DB 2; Length 621;
Pred. No. 3.4e-17;
8; Mismatches 4; Indels
 2; Length 843;
 80.9%; Score 195; DB 2; Length 84 78.3%; Pred. No. 1e-17; ive 6; Mismatches 4; Indels
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
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A;Cross-references: GDB:126565; OMIM:173325
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A;Note: 86E4.6
C;Keywords: cytoskeleton
 78.8%;
73.9%;
 Query Match
Best Local Similarity 78.38
Matches 36; Conservative
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Best Local Similarity 73.9
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 A;Cross-references: GB:M23410
C;Genetics:
 Keywords: cytoskeleton
 A; Molecule type: mRNA
A; Residues: 1-744 <FRA>
 A;Status: preliminary
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Gaps

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Length 806; Indels e F

Length 678;

DB 2;

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3 QEAEMAQNAVRLHYGLPVVVKLLHP-PSHWPLIKATV 38
 Score 56.5; DE pred. No. 11; 4; Mismatches
 Search completed: July 29, 2002, 16:09:18
Job time: 728 sec
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Matches 17; Conservative '
 24.3%;
 Query Match
Best Local Similarity 46.73
Matches 14; Conservative
 A; Start codon: TTG
 A; Map position: 5L
 298
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 RESULT 13
FP90409
FP90409
FP90409
FP90409
C;Species: Sulfolobus solfataricus
C;Species
 Aypothetical protein Y105C5B.s - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
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C; Accession: 726395
R; MCMurray, A.
Submitted to the EMBL Data Library, September 1999
A; Reference number: 220208
A; Rocession: 726395
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rocession: 1-1050 <WIL>
A; MOLEOSE : 1-1050 <WIL>
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A; Experimental source: clone Y105C5B
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A; Gene: CESP:Y105C5B.s
A; Introns: 40/3; 105/1; 217/3; 278/1; 422/1; 482/1; 850/1; 903/1; 959/2
 1;
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 A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-351 <KUR>
A;Cross-references: GB:AE006641; NID:g13815687; PIDN:AAK42533.1; GSPDB:GN00155
C;Genetics: A;Gene: SSO2385
 ij
 VAC8 protein - yeast (Saccharomyces cerevisiae)
N,Alternate names: protein YELOllaw
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Spate: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 29-Oct-1999
 Gaps
 Gaps
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 1;
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 Length 1050;
 Length 351;
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 Indels
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 A; Description: Sulfolobus solfataricus complete genome. A; Reference number: A99139
A; Accession: F90409
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Best Local Similarity 41.7%; Pred. No. 3.8;
Matches 15; Conservative 9; Mismatches 11;
 |||: ||||:|||||:
807 AVRVEKGLPVLVELIRLPEDF-VVCAVATALRNLAI 841
43.5%; Pred. No. 0.024;
iive 7; Mismatches 1
 11 AVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 5; Mismatches
 120 VQIQLVNPPKSLPLSK-TIGLIRN 142
 20 VVVKLLHPPSHWPLIKATVGLIRN 43
 24.7%;
 Conservative
 Best Local Similarity 43.5
Matches 20; Conservative
 Query Match
Best Local Similarity
Matches 13; Conserv
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13; Indels

Length 393;

DB 1;

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C; Species: Methanococcus jannaschii
C; Species: Methanococcus jannaschii
C; Species: Methanococcus jannaschii
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Caccession: E64485
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak J; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, J. Sen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A,Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A,Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A, Reference number: A64300; MuID:96337999
 A; Pathway: purine nucleotide biosynthesis
A;Note: "cofactor magnesium
C; Superfamily: phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain C; Superfamily: phosphoribosylaminoimidazole biosynthesis; transferase
C;Keywords: magnesium; purine nucleotide biosynthesis; transferase
F;29-371/Domain: phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation cha
 A, Description: catalyzes the production of beta-formyl glycinamide ribonucleotide fro
 A;MOJecule type: DNA
A;Reaidues; 1-578 <DIE>
A;Cross_references: EMBL:U18530; NID:g602367; PID:g602380; GSPDB:GN00005; MIPS:VEL013
 A;Cross-references: GB:U67589; GB:L77117; NID:92826417; PIDN:AAB99496.1; PID:91592123
C;Genetics:
 A; Description: required for vacuole inheritance and protein targeting from the cytopl C; Keywords: yeast vacuole
submitted to the EMBL Data Library, December 1994
A; Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495
A; Reference number: S50428
A; Accession: S50446:
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 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues; 1-393 <BUL>
 Length 578;
 Indels
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 DB
 7; Mismatches
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A;Gene: SGD:VAC8; MIPS:YEL013w
A;Cross-references: SGD:SQ000739; MIPS:YEL013w
 293 GLPHLVKLIQSDS-IPLVLASVACIRNISI 321
 17 GLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 A; Map position: REV1458908-1457727
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 29, 2002, 16:09:56 ; Search time 34.24 Seconds (without alignments) 52.018 Million cell updates/sec Run on:

US-09-641-104A-12
241
1 RHQEAEMAQNAVRLHYGLPV.....PPSHWPLIKATVGLIRNLAL 46 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | P35222 homo sapien | _              | Q9wu82 rattus norv | P26233 xenopus lae |            | P35223 tripneustes | P30998 xenopus lae |                | P18824 drosophila |            | P14923 homo sapien |            | 097422 drosophila | -          |            |            | -         | Q59754 rhizobium m | _          | P19028 feline immu | Q09778 schizosacch | 000192 homo sapien | _          | Q9kOnO neisseria m | _          |            | P22221 flaveria tr |            | 2736       | ~         |      | P57136 buchnera ap | P77500 escherichia |
|-----------|---------------|--------------------|----------------|--------------------|--------------------|------------|--------------------|--------------------|----------------|-------------------|------------|--------------------|------------|-------------------|------------|------------|------------|-----------|--------------------|------------|--------------------|--------------------|--------------------|------------|--------------------|------------|------------|--------------------|------------|------------|-----------|------|--------------------|--------------------|
| SUMMARIES | ID            | CTNB_HUMAN         | CTNB_MOUSE     | CTNB_RAT           | CTNB_XENLA         | CTNB_URECA | CTNB_TRIGR         | PLAK_XENLA         | ARM_MUSDO      | ARM_DROME         | PLAK_MOUSE | PLAK_HUMAN         | VAC8_YEAST | B3GT_DROME        | PURT_METJA | PETD_SYNP2 | UBIB_NEIMA | PEX_MOUSE | PODK_RHIME         | PODK_ENTHI | POL_FIVSD          | YA8D_SCHPO         | ARVC_HUMAN         | ARVC_MOUSE | UBIB_NEIMB         | PODK_MESCR | PODK_FLABI | PODK_FLATR .       | PODK_FLABR | PODK_FLAPR | PEX_HUMAN | Γ÷.  | Y023_BUCAI         | YFER_ECOLI         |
|           | DB            |                    | <del>, ,</del> |                    | -                  | -          |                    | -4                 | <del>, -</del> | ٦                 | 7          | 7                  | 7          | -                 | П          | -          | _          | П         | -                  | П          | 7                  | П                  | П                  | П          | _                  | _          | -          | -                  | 7          | -          | -         | -    | -                  | 1                  |
|           | Length        |                    | 781            | 781                | 781                | 818        | 820                | 738                | 813            | 843               | 621        | 743                | 578        | 313               | 393        | 160        | 503        | 749       | 868                | 882        | 1124               | 899                | 962                | 696        | 503                | 949        | 953        | 953                | 955        | 926        | 749       | 1124 | 191                | 308                |
| dР        | ery           | 0                  |                |                    |                    | 90.5       |                    |                    | 82.2           |                   |            |                    |            |                   | 23.4       |            | 22.8       | •         |                    | ٠          |                    |                    |                    |            | ٠                  |            |            |                    | ٠          |            |           | 21.4 |                    | 21.2               |
|           | Score         | 241                | 241            | 241                | 241                | 218        | 202                | 201                | 198            | 195               | 190        | 190                | 58.5       | 56.5              | 56.5       | 55.5       | 52         | 52        | 52                 | 54         | 24                 | 53.5               | 53.5               | 53.5       | 23                 | 53         | 53         | 53                 | 53         | 53         | 52        | 51.5 | 21                 | 21                 |
|           | Result<br>No. | 1                  | 7              | ю                  | 4                  | S          | 9                  | 7                  | ω.             | σ                 | 10         | 11                 | 12         | 13                | 14         | 15         | 16         | 17        | 18                 | 19         | 20                 | 21                 | 22                 | 23         | 24                 | 25         | 56         | 27                 | 28         | 29         | 30        | 31   | 35                 | 33                 |

| Q06965 rhodobacter<br>Q84293 human papil | P03113 human papil<br>079676 pelomedusa | Q09889 schizosacch<br>P58333 rhizobium m | P54787 saccharomyc<br>P17972 drosophila | Q9pce8 xylella fas<br>O14981 homo sapien | Q15332 homo sapien |       |
|------------------------------------------|-----------------------------------------|------------------------------------------|-----------------------------------------|------------------------------------------|--------------------|-------|
| HEMO_RHOSH<br>VE1 HPV6A                  | VE1_HPV6B<br>COX3_PELSU                 | YC9F_SCHPO<br>TKT1_RHIME                 | VPS9_YEAST<br>CIKW DROME                | UBIB_XYLFA<br>T172_HUMAN                 | C11X_HUMAN         |       |
|                                          |                                         |                                          |                                         |                                          |                    | 1     |
|                                          | 2 649<br>0 261                          | •                                        | •                                       | ••                                       | -                  |       |
| 21.                                      | 21.2 $21.0$                             | 21.                                      | 20:                                     | 20.                                      | 200                | ;     |
|                                          | 36. 51 2                                |                                          |                                         |                                          | 44 4 49.5          | ·<br> |

# ALIGNMENTS

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 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 MEDLINE-97442350; PubMed-9298899;
Huber A.H., Nelson W.J., Weis W.I.;
"Three-dimensional structure of the armadillo repeat region of beta-
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 InterPro; IPR00225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARW; 11.
PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein; Repeat; 3D-structure.
 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 118-149 IN COMPLEX WITH
 .;
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 MEDLINE-92376536; PubMed-1509266; Butz S., Stappert J., Weissig H., Kemler R.; "Plakoglobin and beta-catenin: distinct but closely related."; Science 257:1142-1144(1992).
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 "Regulation of beta-catenin signaling in the Wnt pathway.";
Blochem. Biophys. Res. Commun. 268:243-248(2000).
 474 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 519
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 CB78F165A3EEF86E CRC64;
 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 150-665
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 PRT;
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MEDLINE-20145417; PubMed=10679188;
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 STANDARD;
 catenin.";
Cell 90:871-882(1997).
 PIR; S31988; S31988.
PDB; 1G3J; 17-JAN-01.
TRANSFAC; T02872; -.
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 SEQUENCE FROM N.A.
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 Beta-catenin.
CTNNB1 OR CATNB.
 MIM; 116806;
 Kikuchi A.;
 CTNB_MOUSE
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SEQUENCE
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 CTNB_MOUSE
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THE ADDITION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN MOINT CELL SISS-543 (2000).

- FERCATION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF TS. SUBJECT OF THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF THE CYTOSOLIC FORM HOUSE OF THE STIMULATION OF THE CYTOSOLIC FORM HOUSE OF THE ALSO BIND CONTINES AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND CONTINES AND DUPLIN. CAN HETERODIMERIZE WITH ALCHA-CATENIN AND CONTINES AT THE ANCHORAGE OF THE CADHERIN COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN CAPOSPHORYLATION).

- SUBJECTION OF THE CADHERIN COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF STABILIZED (LOW LEVEL OF PHOSPHORYLATION).

- STABILIZED (LOW LEVEL OF PHOSPHORYLATION) OF SETA-CATENIN IS REDUCED AND THE PROTEIN IS NO LONGER DEGRADED, CONTINING IN THE ACCUMULATION IN CYTOPLASM.

- RESULTING IN ITS ACCUMULATION IN CYTOPLASM.

- STAILLARITY: BELONGS TO THE BETA-CATENIN FAMILY.
 ö
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 Gaps
 PIR; S35041; S35041.
PDB; 38CT; 15-0CT-97.
PDB; 38CT; 19-NOV-97.
PDB; 1DOW; 12-JUL-00.
PDB; 1DOW; 12-JUL-00.
INTERNEFAC; 702984; ...
MGI: 88276; Catnb.
Interpro; IPR000225; Armadillo_seg; 12.
SMART; SM00185; ARM, 11.
PROSITE; PS50176; ARM, REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
 of
 ö
 Pokutta S., Weis W.I.; "structure of the dimerization and beta-catenin-binding region
 Length 781;
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 D708F170A3FBED6E CRC64;
 100.0%; Score 241; DB 1; 100.0%; Pred. No. 2.7e-24;
 A.
 0; Mismatches
 781
 PRT;
MEDLINE-20337986; Pubmed-10882138;
 ARM
ARM
ARM
ARM
ARM
ARM
ARM
ARM
 781'AA; '85470 MW;
 EMBL; M90364; AAA37280.1; -.
 46; Conservative
 STANDARD;
 Local Similarity
 100
147
189
 alpharcatenin.
Möl* Cell 5:53
 Repeat; 3D-st
REPEAT
 $35091;
 SEQUENCE
 Query Match
 CINB_RAT
 REPEAT
REPEAT
REPEAT
 REPEAT
REPEAT
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4. RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 519 #1, RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46

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 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 J. Cell. Physiol. 181:258-272(1999).

-! FUNCTION: INVOLVED IN THE REGULATION OF CELL ADHESION AND IN SIGNAL TRANSDUCTION THROUGH THE WWY PATHWAY (BY SIMILARITY).

-! SUBUNIT: THE CYTOSOLIC FORM BOUND TO AXIN ALLOWS THE STIMULATION OF ITS DEGRADATION. THE CYTOSOLIC FORM ALSO INTERACTS WITH APC AND E-CADHERIN. THE MUCLEAR FORM BINDS TCF/LEF-1 AND MAY ALSO BIND PONTINS2 AND DUPLIN. CAN HETERODIMERIZE WITH ALPHA-CATENIN AND ALSO FORM A TRIMERIC COMPLEX WITH CADHERIN. MEDIATES THE ANCHORAGE OF THE CADHERIN COMPLEX TO THE CORTICAL ACTIN CYTOSKELETON (BY
 STRAIN-SPRAGUE-DAWLEY, TISSUE-Testis;
MEDLINE-99428593; PubMed-10497305;
Chung S.S.W., Lee W.M., Cheng C.Y.;
"Study on the formation of specialized inter-Sertoli cell junctions in
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
 9C29186B6DD54B87 CRC64;
 Last sequence update)
Last annotation update)
 4.0.67.89
 ARM
ARM
ARM
ARM
ARM
ARM
ARM
 InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
 Created)
 EMBL; AF121265; AAD28504.1; -. HSSP; Q02248; 2BCT.
 85454 MW;
16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 01-MAR-2002 (Rel. 41,
 Query Match
Best Local Similarity
 637
781 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 SMART; SM00185;
 Beta-catenin
 SEQUENCE
 Repeat.
REPEAT
 REPEAT
REPEAT
 REPEAT
 REPEAT
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 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
 Gaps
 SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL ADHESION PROPERTIES: ESSENTIAL COMPONENT OF THE VERTEBRATE WNT-SIGNALING PATHWAY AND IS REQUIRED FOR FORMATION OF THE EMBRYONIC AXIS.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 Science 254:1359-1361(1991).

-!- FUNCTION: BINDS TO THE CYTOPLASMIC DOMAIN OF THE CELL-CELL ADHESION WOLECULE E-CADHERIN. AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATERINS TO CADHERINS PRODUCES A COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WH
 McCrea P.D., Turck C.W., Gumbiner B.M.; "A homolog of the armadillo protein in Drosophila (plakoglobin) associated with E-cadherin.";
 ö
 Length 781;
 Indels
 Structural protein; Repeat.
 3ECD27232239F799 CRC64;
 SIMILARITY: BELONGS TO THE BETA CATENIN FAMILY.
SIMILARITY: CONTAINS 10 ARM REPEATS.
 100.0%; Score 241; DB 1;
100.0%; Pred. No. 2.7e-24;
iive 0; Mismatches 0;
 01:WAY-1992 (Rel. 22, Created)
01:WAY-1992 (Rel. 22, Last sequence update)
01:WAR-2002 (Rel. 41, Last annotation update)
 781 AA
 SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
 Xenopús laevis (African clawed frog).
 PRT;
 MEDLINE=92073903; PubMed=1962194;
 ARM
ARM
ARM
ARM
ARM
 ARM
 ARM
 Pfam; PF00514; Armadillo_seg; 12.
 ο,
 InterPro; IPR000225; Armadillo.
 PROSITE; PS50176; ARM REPEAT;
Cell adhesion; Cytoskeleton; S
 85449 MW;
 EMBL; M77013; AAA49670.1; -. PIR; S35099; S35099.
 Conservative
 STANDARD;
 SMART; SM00185; ARM; 11
 306
 Xenopus.
 Local Similarity
 584
625
781 AA;
 2BCT.
 HSSP; Q02248; 2BC
TRANSFAC; T03026
 NCBI_TaxID=8355,
 Beta:catenin.
 TISSUE-Brain,
 Xenopodinae;
 Matches 46;
 CTNB_XENLA
 REPEAT
SEQUENCE
 Query. Match
 REPEAT
REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
CTNB_XENLA
 Best
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1 RHOBABAMAONAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNIAL 46

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Gaps

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Length 781; Indels

100.0%; Score 241; DB 1; 100.0%; Pred. No. 2.7e-24; iive 0; Mismatches 0;

Conservative

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 "Identification of homologues to beta-catenin/plakoglobin/armadillo in two invertebrates, Urechis caupo and Tripneustes gratilla."; Biochim. Brown Nolecule E-Cadherin, AND PERHAPS TO GTHER (MEMBRANE) PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A COMPLEX WHICH IS LINEED TO THE ACTIN FILAMENT NETWORK, AND WHICH SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
 Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III).
5. Seropus laevis (African clawed frog).
Eukaryota; Metazoa; Chordeat (Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Score 202; DB 1; Length 820; Pred. No. 4.2e-19;
 Structural protein; Repeat.
 490 RHPGAEMGONTVRLNYGIPVIVKLLHPPSRWPLIKATVGLIRNLAL 535
 57255E0F57795FD3 CRC64;
 . . 1 . RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL
 PROPERTIES.

-1; SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-1; SIMILARITY: CONTAINS 10 ARM REPEATS.
 738 AA
 Mismatches
 FIRST, COC246; IDOW.
InterPro; IPR000225; Armadillo.
Prém; PF0014; Armadillo_seg; 12.
SMART; SM00185; ARW: 12.
PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Struct
 ARM 3.
ARM 4.
ARM 5.
ARM 7.
ARM 8.
ARM 9.
 SEQUENCE FROM N.A.
MEDLINE-93305730; PubMed-8318544;
 ARM
 89361 MW;
 83.8%;
ilarity 82.6%;
Conservative
 EMBL; L10354; AAA30089.1; -.
 · STANDARD;
 233
280
322
445
485
 Xenopus.
 S33794; S33794.
 Best Local Similarity
Matches 38; Conserv
 820 AA;
 [1]. SEQUENCE FROM N.A.
 NCBI_TaxID=7673;
 NCBI_TaxID=8355;
 Rosenthal E.T.;
 xenopodinae;
 lripneustes
 PLAK_XENLA
P30998;
 REPEAT
SEQUENCE
 Query Match
 REPEAT
REPEAT
 REPEAT
 REFEAT
 REPEAT
 REPEAT
 REPEAT
 RESULT 7
PLAK_XENLA
 REPEAT
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 ö
 Gaps
 SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
 ;
0
 Urechis caupo (Innkeeper worm) (Spoonworm).
Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
NCBI_TaxID=6431;
 Length 818;
 Score 218; DB 1; Length 81. Pred. No. 3.2e-21;
 Structural protein; Repeat.
 474 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 519
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 1DF174BEEF745C1D CRC64;
 SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS 7 ARM REPEATS.
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 820 AA
 1; Mismatches
 Tripneustes gratilla (Hawaian sea urchin).
 ARM 1.
ARM 2.
ARM 4.
ARM 5.
ARM 6.
 MEDLINE-93305730; PubMed-8318544; Rosenthal E.T.;
 HSSP; Q02248; 2BCT.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SMOIDS5; ARW, 11.
PROSITE; PS50176; ARW_REPEAT; 9.
Cell adhesion; Cytoskeleton; Stru
 89070 MW;
 90.5%;
91.3%;
 EMBL; L10355; AAA30330.1; -.
 Query Match
Best Local Similarity 91.3
Matches 42; Conservative
 STANDARD;
 STANDARD;
 451
495
 818 AA;
 SEQUENCE FROM N.A.
 PROPERTIES
 Beta-catenin.
 Beta-catenin.
 01-FEB-1994
01-FEB-1994
 CTNB_TRIGR
P35223;
 CTNB_URECA
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Gaps

; 0

Indels

46

SEQUENCE

CTNB\_TRIGR

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REPEAT

REPEAT REPEAT REPEAT

REPEAT

CTNB\_URECA
AC GYANB\_UA
AC GA
AC GYANB\_UA
AC GA
AC GA
AC GYANB\_UA
AC GA
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REPEAT REPEAT

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 Muscardomestica (House fly).
Bukařýota, Metazos, Atthropoda, Tracheata, Hexapoda, Insecta,
Ptérygota, Neoptera, Bindopterygota, Diptera, Brachycera, Muscomorpha,
Muscoldea, Muscidáe, Musca
 Peifer M.A., Wieschaus E.;
"The:product of the Drosophila melanogaster segment polarity gene
armadillo is highly conserved in sequence and expression in the
 PROSITE; PS50176; ARM_REPEAT; 9.
Developmental protein; Repeat;
Cell adhesion; Cytoskeleton; Structural protein.
DOMAIN 1 148 ASP/GLU-RICH (ACIDIC).
 4; Indels
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 73E61F59BDBFA580 CRC64;
 782.2%; Score 198; DB 1; 78.3%; Pred. No. 1.4e-18;
 01:JUL-1993 (Rel::26, Created)
01:JUL-1993 (Rel::26, Task sequence update)
01:JURA-2002 (Rel::41, Last annotation update)
Armadillo segment polarity protein.
 P1E824; 002371; 09W546; 01sNOY-1990 (Rel. 16, Created) (Nel. 16, Last sequence update) 01:WOY-1990 (Rel. 41; Last sequence update) 01:WAR-2002 (Rel. 41; Last annotation update)
 843 AA
 6; Mismatches
 PRT;
 ARM 1.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 8.
 MEDLINE=93247062; PubMed=8483160;
 Pfam; TPF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; 11.
 ARM
 EMBL;:L04874; AAA29292.1; --
HSSP;:Q02248; 1DOW.
Interpro; IPR000225; Armadillo.
 88237 MW;
 36; Conservative
 STANDARD;
 SEQUENCE FROM N.A:
 813:AA;
 Best Local Similarity
 NCBI_TaxID=7370;
01÷JUE-1993
 ARM_DROME
 SECUENCE
 Query Match
 REPEAT
REPEAT
 REPEAT
REPEAT
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REPEAT
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 REPEAT
 RESULT 9
 Matches
 ARM_DROME
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 DA PEP
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 ó
 Gaps
 DEV. BIOI. 153:337-346(1992).

-1- FUNCTION: COMMON JUNCTIONAL PLAQUE PROPEIN. THE MEMBRANE-ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION OF BOTH THE CYTOSKELETON AND THE CELLS MITHIN THE TISSUE. THE PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
 Fouquet B., Zimbelmann R., Franke W.W.; "Identification of plakoglobin in oocytes and early embryos of Xenopus laevis: maternal expression of a gene encoding a junctional
 SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
 ö
 MEDLINE-93012479; PubMed-1397690; de Marais A.A., Moon R.T.; "The armadillo homologs beta-catenin and plakoglobin are differentially expressed during early development of Xenopus
 Length 738;
 Indels
 Structural protein; Repeat.
 -> V (IN REF. 2).
-> T (IN REF. 2).
569DBE69D08BBC58 CRC64;
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 ASSOCIATED FORM.
-!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-!- SIMILARITY: CONTAINS 10 ARM REPEATS.
 Pred. No. 5.2e-19;
8; Mismatches 3;
 83.4%; Score 201; DB 1; 76.1%; Pred. No. 5.2e-19;
 or send an email to license@isb-sib.ch).
 ARM 2.
ARM 4.
ARM 5.
ARM 6.
ARM 6.
ARM 9.
ARM 9.
 MEDLINE=93093332; PubMed=1459359;
 ARM
 InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11
 Differentiation 51:187-194(1992)
 PROSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Str
REPEAT 128 167
 81711 MW;
 SEQUENCE OF 133-292 FROM N.A
 EMBL; M95593; AAA49931.1; -.
 EMBL; X67078; CAA47463.1; -. PIR, S24636; S24636; PIR, S35093; S35093. HSSP; Q02248; 2BCT.
 Conservative
 SMART; SM00185; ARM; 10
 Query Match
Best Local Similarity
Lagar 35; Conserve
 226
738 AA;
 plaque protein.";
 CONFLICT
 CONFLICT
 laevis.
 REPEAT
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Gaps

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PRT;

STANDARD;

ARM\_MUSDO

ARM\_MUSDO RESULT SG

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õ g 002453;

Length 813;

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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Bacton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Button G.G., Mortnan J.R., Mantels B.G., Malson C.R., Miklos G.L.G.,
RA Bellew R.W. Basud A. A. Baxendale J., Bayraktaroglu L., Bealey B.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakor S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakor S.,
RA Berry J.M., Cawley S., Dahlke C., Davenpour L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpour L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpour L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischman W.,
RA Barlis K.J., Evongelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RA Glodek A., Gong F., Gorrell J. H., Calbart W., Clabaser K.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kunp D., Liai Z.,
Liako P., Lei Y., Levitsky A.A., Lii J., Liang Y., Lin X.,
Alako M., Marphy B., Murphy L., Murzny D.M., Nelson D.L.,
Merkluv G. M. Ishina N.V., Mobarry C., Morris J., Morler S., Smith T.,
Shue B.C., Siden-Klamos I., Simpson M., Skrupski M.P., Smith T.,
Shue B.C., Siden-Klamos I., Simpson M., Skrupski M.P., Smith T.,
Ra Spier E., Spradling A.C., Stapleton M., Zhong G., Zhoo O., Zheng L.,
Ra Spier E., Spradling A.C., Stapleton M., Zhong G., Zhoo O., Zheng L.,
Ra Shier S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho O.,
Ra Spier E., Shorel E.W., Rubin G.M., Welnet E.,
Ra Gibbs R.A., Woodage T., Worley K.C., Wu D., Yang S., Zho O.,
Ra Haris R.H., Permone G. Prockophila melanogaster.";
R. The genome Sequence of Drosophila melanogaster.";
Armadillo segment polarity protein.

ARM OR EG:66E4.6 OR CG11579.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
 Riggleman B., Wieschaus E., Schedl P.; "Molecular analysis of the armadillo locus: uniformly distributed transcripts and a protein with novel internal repeats are associated
 MEDLINE-20196011; PubMed-10731137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
 Loureiro J., Peifer M.;
"Roles of Armadillo, a Drosophila catenin, during central nervous
system development.";
 SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND ALTERNATIVE
 with a Drosophila segment polarity gene.";
 SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
 SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
 SEQUENCE FROM N.A. (CYTOPLASMIC ISOFORM).
 MEDLINE=20196006; PubMed=10731132;
 MEDLINE=89211895; PubMed=2707602;
 MEDLINE-98298928; PubMed-9635189;
 "The genome sequence of Dros Science 287:2185-2195(2000).
 Biol. 8:622-632(1998).
 Genes Dev. 3:96-113(1989).
 STRAIN-OREGON-R
 STRAIN-BERKELEY
 rissum-Head;
```

```
RN [5]; "

RD PHOSPHORYLATION.

RP PHOSPHORYLATION.

RA MEDILINE=5813174; PubMed=7529201;

RA MEDILINE=5813174; PubMed=7529201;

RA MEDILINE=5813174; PubMed=7529201;

RA MEDILINE=5813174; PubMed=7529201;

RT Phosphorylation of the Drosophila adherens junction protein

RT Admadillo: roides for windless signal and zeste-white 3 kinase.";

RT Admadillo: roides for windless signal and zeste-white 3 kinase.";

RT Admadillo: roides for windless signal and zeste-white 3 kinase.";

RT Admadillo: roides for windless signal and zeste-white 3 kinase.";

RT Admadillo: roides for benebower for Benebower AccountLates THROUGH WG

CC SIGNALING. ARM FUNCTION IN WG SIGNAL TRANSDUCTION. CAN ASSOCIATE

CC SIGNALING. ARM FUNCTION IN WG SIGNAL TRANSDUCTION IS REQUIRED

CC SIGNALING. AND BEPIDERMIS.

CC STOPELAMINE TRANSMISSION OF DETERMINATION OF NEUROBLAST FATE. ARM AND

ABL PROTEINS FUNCTION COOPERATIVELY AT ADHERENS JUNCTIONS IN BOTH

CC STOPE STORE STORE OF CELL MEMBRANE.

CC STORE SUBCECTION STORE STORE STORE STORE STORE STORE STORE

CC STORE SPECIFICITY: CYTOPLASMIC ISOFORM IS PREDOMINANT BEFORE

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 Borkova D.,
 EMBRYONIC TISSUE TO TISSUE. SGG IS REQUIRED FOR PHOSPHORYLATION AND WG SIGNAL NEGATIVELY REGULATES ARM PHOSPHORYLATION.

AND WG SIGNAL NEGATIVELY REGULATES ARM PHOSPHORYLATION.

SIMILARITY: BELONGS TO THE BETA-CATININ FAMILY.

SIMILARITY: CONTAINS 12.5 ARM REPEATS.
Dream S., Gloux S., Lelaure V., Mottler S., Gallbert F., Borkova Minana B., Kafatos F.C., Louis C., Siden-Klamos I., Bolshakov S., Pabagajannakis G., Spaños L., Cox S., Madueno E., de Pablos B., Modolall J., Peter A., Schoettler P., Werner M., Mourkloti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 PROSITE; PS50176; ARM REPEAT; 9.
Developmental protein; Segmentation polarity protein; Repeat; Cell; adhesion; Cytoskeleton; Structural protein; Phosphorylation;
 'From sequence to chromosome: the tip of the X chromosome of D.
 Interpro; IPR000225; Armadillo.
Pfam; PF00514;: Armadillo_seg; 12.
 Science 287:2220-2222(2000).
 EMBL; X54468; CAA38350.1; -.
 FlyBase; FBgn0000117; arm
 SMART; SM00185; ARM;
 Cell, adhesion; Cytosk
Alternative splicing.
 T02977
 HSSP; 002248;
TRANSFAC; T02
 melanogaster.
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REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 PLAK_HUMAN
 Matches
 RESULT
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 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 EMBL outstation
 GLEISSPVGGGAGGAPGNGGAVGGASGGGGNIGAIPPSGA
PREYSKMANDWOTGEIDAGALKFULDAMFTPPNDNNNLAAWYD
TDC -> ILYQ (IN NEURAL ISOFORM).
40DAD6FB83163049 CRC64;
 ASP/GLU-RICH (ACIDIC).
LGPEEAYEGLYGQGPPSVHSSHGGRAFHQQGYDTLPIDSMQ
 Gaps
 Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMMON JUNCTIONAL PLAQUE PROPEIN. THE MEMBRANE-
ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT
STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION
OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE
PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE
INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CERTRAL ROLE IN
THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-ASSOCIATED FORM.
 ö
 MEDLINE-92277536; PubMed-1509266; Butz S., Stappert J., Weissig H., Kemler R.; "Plakoglobin and beta-catenin: distinct but closely related.";
 Length 843;
 the Swiss Institute of Bioinformatics and the
 Indels
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. SIMILARITY: CONTAINS AT LEAST 9 ARM REPEATS.
 ASP/GLU-RICH (ACIDIC)
 01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Junction plakoglobin (Desmoplakin III) (Fragment).
 ARM 3.
ARM 4.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
ARM 9.
ARM 9.
ARM 10.
ARM 11.
ARM 11.
ARM 11.
 Score 195; DB 1;
Pred. No. 3.7e-18;
5; Mismatches 4;
 ;
9
 01-JUL-1993 (Rel. 26, Created)
 91152 MW;
 80.98;
78.38;
 Science 257:1142-1144(1992).
 REVISIONS TO 294 AND 296.
 Conservative
 STANDARD;
 musculus (Mouse)
 843 AA;
 Query Match
Best Local Similarity
Matches 36; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 243
285
327
369
369
4111
539
 PLAK_MOUSE
Q02257;
 DOMAIN
VARSPLIC
 SEQUENCE
 petween
 REPEAT
REPEAT
 RPEAT
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 REPEAT
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 PLAK_MOUSE
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 ö
 "Molecular cloning and amino acid sequence of human plakoglobin, the common junctional plaque protein.";

Prico. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989).

-:- FUNCTION: COMMON JUNCTIONAL PLAQUE PROTEIN. THE MEMBRANE-ASSOCIATED PLAQUES ARE ARCHITECTURAL ELEMENTS IN AN IMPORTANT STRATEGIC POSITION TO INFLUENCE THE ARRANGEMENT AND FUNCTION OF BOTH THE CYTOSKELETON AND THE CELLS WITHIN THE TISSUE. THE PRESENCE OF PLAKOGLOBIN IN BOTH THE DESMOSOMES AND IN THE INTERMEDIATE JUNCTIONS SUGGESTS THAT IT PLAYS A CENTRAL ROLE IN
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 SUBCELLULAR LOCATION: CYTOPLASMIC IN A SOLUBLE AND MEMBRANE-
 ;
0
 Length 621;
 Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M., Schiller D.L., Cowin P.;
 4; Indels
 PRÖSITE; PS50176; ARM_REPEAT; 9.
Cell adhesion; Cytoskeleton; Structural protein; Repeat.
 THE STRUCTURE AND FUNCTION OF SUBMEMBRANOUS PLAQUES. SUBUNIT: HOMODIMER.
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 17CF444607422BAA CRC64;
 ASSOCIATED FORM.
-!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
-!- SIMILARITY: CONTAINS 8 ARM REPEATS.
 Score 190; DB 1;
Pred. No. 1.2e-17;
 01-APR-1990 (Rel. 14, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Junction plakoglobin (Desmoplakin III).
 Ş
 8; Mismatches
or send an email to license@isb-sib.ch).
 ARM 1.
ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 7.
 MGD; MGI:96650; Jup.
InterPro; IPRO00225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARM; 8.
 MEDLINE-89264555; PubMed-2726765;
 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seq
01-MAR-2002 (Rel. 41, Last anno
 MW.
 78.8%;
73.9%;
 EMBL; 1 M90365; AAB02885.1; -.
 68111
 34; Conservative
 STANDARD;
 131
173
257
296
 340
386
427
 . S35092.
 Homo sapiens (Human).
 450
621 AA;
 1DOW
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 PIR; S35092; S
HSSP; Q02248;
 PLAK_HUMAN
P14923;
 JUE OR DE3
 Query Match
Best Local S
 SEQUENCE
 NON_TER
REPEAT
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578 AA;
 SEQUENCE FROM N.A.
 76
116
1157
1198
2239
323
 melanogaster.
 Glover D.M.;
 B3GT_DROME
 REPEAT
SEQUENCE
 Query Match
 REPEAT
REPEAT
REPEAT
 REPEAT
REPEAT
 REPEAT
 RESULT 13.
 REPEAT
 REPEA
 Best Loca
Matches
 B3GT DROME
 qq
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 ;
0
 sits content is in no way Usage by and for commercial
 Gaps
 -1- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY. MOST SIMILAR TO PLAKOGLOBINS.
-1- SIMILARITY: CONTAINS 9 ARM REPEATS.
 Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guzanan E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petell F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelcon M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 GQLA -> DSSL (IN REF. 1; AAA64895).
V -> A (IN REF. 1; AAA64895).
472741F400D388FD CRC64;
 Wang Y.X., Catlett N.L., Weisman L.S.;
Unpublished observations (XXX-1997).
-!- FUNCTION: FUNCTIONS IN BOTH VACUOLE INHERITANCE AND PROTEIN
TARGETING FROM THE CYTOPLASM TO VACUOLE.
 ö
 78.8%; Score 190; DB 1; Length 743; 73.9%; Pred. No. 1.5e-17;
 Indels
 protein; Repeat.
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 4
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 578 AA
 8; Mismatches
 Saccharomyces cerevisiae (Baker's yeast).
 Structural PROBABLE.
send an email to license@isb-sib.ch)
 ARM 1.
ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 5.
ARM 6.
 PRT;
 InterPro; IRR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 10.
SMART; SM00185; ARM; 8.
PROSITE; PS50176; ARM_REPEAT; 8.
Cell adhesion; Cytoskeleton; Struct
INIT_MET
 81498 MW;
 EMBL; M23410; AAA64895.1; -.
 Best Local Similarity 73.9
Matches 34; Conservative
 STANDARD;
 Vacuolar protein 8.
VAC8 OR YEL013W.
 PIR; A32905; A32905
 HSSP, Q02248; 2BCT MIM; 173325; -.
 743 AA;
 SEQUENCE FROM N.A.
 CHARACTERIZATION
 NCBI_TaxID=4932;
 VAC8_YEAST
P39968;
 Query Match
 SEQUENCE
 CONFLICT
 REPEAT
 REPEAT
 REPEAT
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 REPEAT
 REPEAT
 REPEAT
 EAST
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entities requires'a license agreement (See http://www.lsb-sib.ch/announce/
or:send an email to license@lsb-sib.ch).
 ä
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryjota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Gaps
 Bariell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Minana B., Kafatos F.C., Louis C., Siden-Klamos I., Bolshakov S., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A./-Schoeftler P., Werner M., Mourklott F., Beinett N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Campbell L.A., Darlamitsou A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 xylosylprotein.
-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 43.
 "From'sequence to chromosome: the tip of the X chromosome of D.
 ij
 Length 578;
 Indels
 B2E75774B47E5933 CRC64;
 8
 1;
 16-0CT-2001 (Rel..40, Last sequence update)
Probable glucuronosyltransferase (EC 2.4.1.135).
EG:EG0007.5.
 DB
 313 AA
 24.3%; Score 58.5; Di
46.7%; Pred. No. 3.3;
vative 7; Mismatches
 293 GLPHLVKLIQSDS-IPLVLASVACIRNISI 321
 17 GLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 STRAIN-Oregon-R;
MEDLINE-20196011; PubMed-10731137;
 ARM
ARM
ARM
ARM
ARM
ARM
 SGD; $0000739; VAC8
Interpro; IPR000225; Armadillo.
SMART; SMO0185; Armadillo_seg; 9.
SMART; SMO0185; ARM; 8.
PRÓSITE; PS50176; ARM; REPEAT; 7.
Cytoskeleton; Repeat:
 [6-OCT-2001 (Rel. 40, Created)
[6-OCT-2001 (Rel. 40, Last seques of the content o
 63207 MW;
 EMBL; (U18530; AAB64490.1; -.
 Local Similarity 46.7
 :STANDARD;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/orksend an email to license@isb-sib.ch).
 InterPro; IPR000179; Cyt_b_b6.
 Query Match 23.4%;
Best Local Similarity 45.9%;
Matches 17; Conservative 4
 EMBL; X63049; CAA44775.1; -.
 EMBL; U67589; AAB99496.1; -.
 ilarity 31.4%;
Conservative
 STANDARD;
 Query, Match
Best Local Similarity
Matches 16, Conserva
 .
 PIR; S18124; S18124.
PIR; S26194; S26194
 SEQUENCE FROM N.A.
 NCBI_TaxID=32049;
 TIGR; MJ1486;
 PETD_SYNP2
 SEQUENCE
 PETD_SYNP2
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 (See http://www.isb-sib.ch/announce/
 STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-9633999; Pubmed-86808087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Werrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
 FUNCTION: CATALYZES TWO REACTIONS: THE FIRST ONE IS THE PRODUCTION OF BETA-FORMYL GLYCINAMIDE RIBONUCLEOTIDE (GAR) FROM FORMATE, ATP AND BETA GAR; THE SECOND, A SIDE REACTION, IS THE PRODUCTION OF ACETYL PHOSPHATE AND ADP FROM ACETALE AND ATP (BY SIMILARITY) CATALYTIC ACTIVITY: FORMATE + ATP + 5'-PHOSPHO-RIBOSYLGLYCINAMIDE = 5'-PHOSPHORIBOSYL-N-FORMYLGLYCINAMIDE + ADP + PYROPHOSPHATE (BY
 IN DE NOVO PURINE BIÒSYNTHESIS. THIS IS AN ALTERNATIVE ENZYME TO THE PURN GAR TRANSFORMYLASE (BY SIMILARITY). SIMILARITY: BELONGS TO THE PURK / PURT FAMILY.
 Gaps
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)
(GAR transformylase 2) (5'-phosphoribosylglycinamide
transformylase 2) (Formate-dependent GAR transformylase).
 PATHWAY: THIRD STEP (FIRST OF TWO TRANSFORMYLATION REACTIONS)
 LUMENAL (POTENTIAL).
CATALYTIC BASE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
N-LINKED (GLCARC. . .) (POTENTIAL).
0141DCD4CD778436 CRC64;
 and for
 15;
 DB 1; Length 313;
 64 QKAELTSNA-----PYSNRLSHLFMLLPHLHWIIVEDTNATTPLVRNL 106
 3 QEAEMAQNAVRLHYGLPVVVKLLH-----PPSHWPLIK---ATVGLIRNL 44
 Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 11; Indels
 Usage by
 393 AA
 Pred. No. 3.2;
7; Mismatches
 modified and this statement is not removed
 Score 56.5;
 entities requires a license agreement (or send an email to license@isb-sib.ch)
 PRT;
 35805 MW;
 23.4%;
 Science 273:1058-1073(1996).
 EMBL; AL033125; CAA21824.1;
 Query Match
Best Local Similarity 34.09
Matches 17; Conservative
 Methanococcus jannaschii.
 STANDARD;
 313
259
170
 313 AA;
 NCBI_TaxID=2190;
 30
259
170
97
 SIMILARITY)
 PURT_METJA
 DOMAIN
ACT_SITE
METAL
 CARBOHYD
 SEQUENCE
 PURT_METJA
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 5;
 ä
 Gaps
 Gaps
 MEDLINE-93043038; PubMed-1421151;
Brand'S.N., Tan X:, Widger W.R.;
"Cloning and sequencing of the petBD operon from the cyanobacterium
 Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 3;
 19;
 .23.0%; Score 55.5; DB 1; Length 160; 31.4%; Pred. No. 2.1;
 DB 1; Length 393;
 46
 26
 Indels
 5 AEMAQNAVRLHYGLPVVVKLLHPPSHWP------LIKATVGLIRNLAL
 Indels
 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Cytochrome B6-F complex subunit 4 (17 kDa polypeptide).
InterPro: IPR003135; ATP-grasp.
Pfam; PF02222; ATP-grasp; 1.
Purine blosynthesis; Transferase; Complete proteome.
SEQUENCE 393 AA; 43553 MW; A47801A0277B6B87 CRC64;
 Electron transport; Photosynthesis; Transmembrane.
SEQUENCE 160, AA; 17537 MW; E0D8081AE4CAEBE4 CRC64;
 11;
 13;
 CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.
 298 QEMSEFEIHVRAILGLPVSTKLIHPGASH--VIKAEI 332
 33 QEAEMAQNAVRLHYGLPVVVKLLHP-PSHWPLIKATV 38
 ; Score 56.5; DB
; Pred. No. 4;
4; Mismatches
 160 AA
 5; Mismatches
 Pfam; PF00032; cytochrome_b_C; 1.
PROSIΩE; PS00193; cYTOCHROME_B_QO; 1.
 PRT;
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Search completed: July 29, 2002, 16:09:57 Job time: 762 sec

Q94b70 arabidopsis

Perfect score: Sequence: Scoring table:

Searched:

Database

OM protein

Run on:

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09d294 mus musculu 09g8r8 mysoma viru 09v3l8 drosophila 097059 drosophila 043028 schizosacch 093x8 zea mays (m 093x8 zea mays (m 093x8 zea mays (m 023928 eleocharis 023928 eleocharis 02997 eleocharis 09phpy halobacteri 09fije arabidopsis 038812 rattus norv 09u38 caenorhabdi p90935 caenorhabdi p90935 caenorhabdi p90935 caenorhabdi p90935 caenorhabdi 091081 knomu 09de61 xenopus lae 09182 streptomyce 076283 trypanosoma
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
 .100.0%; Score 241; DB 13; Length 781; .100.0%; Pred. No. 9.7e-25; tive 0; Mismatches 0; Indels 0;
 chicken beta-catenin.";
 InterPro; IPR000225; Armadillo.
Pfam: PF00514; Armadillo_seg; 12.
SWART, SM00185; ARM; 11.
SPG0TIE; PS50176; ARW REPEAT; 8.
SEQUENCE 781:AA; 85438 MW; 6D205D9A4DBAC562 CRC64;
 Last sequence update)
Last annotation update)
 781 AA
 SECUENCE FROM N.A.
STARIN-WHITE LEGHONS, TISSUE-DORSAL SKIN;
MEDLINE-97464068; PubMed-9322759;
Lu J., Chuong C.M., Widelitz R.B.;
"Isolation and characterization of chicken legen 196:201-207(1997).
EMBL; UB2964; AAB80856.1; --
HSSP; P35222; 163J.
 ALIGNMENTS
 Q9D294
Q9Q8R8
Q9V3L8
O97059
 Q93XF3
Q97061
Q23928
 023927
09PCY0
09PNP7
09FV16
035812
09U3A8
P90935
P90936
091081
 076283
022220
Q66972
 Created)
 Q24801
Q9L2C5
 PRT;
 486 ... PRELIMINARY; 042486; PRELIMINARY; 042486; 01:JAN-1998 (TrEMBLREL). 05, C1 01:JAN-1998 (TrEMBLREL). 05, L6 01:DEÇ-2001 (TrEMBLREL). 19, L6
 55
33
10
110
111
111
113
113
113
115
115
 Best Local Similarity 100. Matches 46; Conservative
 спыска.
Gallus gallus (Chicken).
 4448888888888888888844444666
 NCBI_TaxID=9031;
 BETA CATENIN.
Query Match
 CHBCAT.
 RESULT
042486
 1D ACC DDT ACC
 042486 gallus gall 090424 brachydanio 090424 brachydanio 0904144 ciona intes 076152 ciona savig 061529 lytechinus 09byf7 brachydanio 015151 homo sapien P70565 rattus norv 025100 hydra magni 094326 caenorhabdi 0994018 sulfolobus 099425 sulfolobus 090425 musculu 090435 musculu
 (without alignments)
63.969 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 241
1 RHQEAEMAQNAVRLHYGLPV......PPSHWPLIKATVGLIRNLAL
 July 29, 2002, 16:12:11 ; Search time 124.4 Seconds
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 562222 seqs, 172994929 residues
 SUMMARIES

 protein search, using sw model

 042486
090424
090335
090144
076152
061229
09PVF7
0915151
09BWC4
P70565
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 sp_unclassified:*
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sp_human:*
sp_invertebrate:*
 sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su
 sp_bacteriap:*
 sp_organelle:*
sp_phage:*
 US-09-641-104A-12
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 sp_archea:*
sp_bacteria:*
 sp_archeap:*
 4 4 13
 sp_rvirus:*
 sp_mammal:*
sp_mhc:*
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 Length
 Query
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98.8
96.7
96.7
96.7
89.6
89.6
89.6
78.8
78.8
78.8
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78.2
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O22220 arabidopsis Q66972 feline immu O06643 nitrosococc Q9rail nitrosococc

Q9kky5 vibrio chol Q92412 mus musculu

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474 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 519

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044326 090308 09RH13 097W55 09D102

1181 107 351 359

241 233 233 216 216 202 190 190 190 190 188 28.5 59.5 59.5

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1. RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46

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Sužuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.
 Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB031543; BAA92185.1; -.
HSSP; P35222; 1G3J.
 464 RHPDAEMAQNAVRLHYGLPVLVKLLHPPSRWPLIKAVVGLIRNLAL 509
 474 RHQETEMAQNAVREHYGLPVVVKLLHPPSHMPLIKATVGLIRNLAL 519
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
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Pfám; PF00514; Armadillo_seg; 11.
SMART; SM0185; ARM; 11.
PROSTIE; P$50176; ARM_REPERT; 6.
SEQUENCE 769 AA; 84703 MW; F61CC489B436E1BC CRC64;
 FI RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
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Interpro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; ARM REPEAT; 7.
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Last sequence update)
Last annotation update)
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Last annotation update)
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 769 AA
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 Created)
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Best Local Similarity 89.1%;
Matches '41; Conservative
 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 09, 01-DEC-2001 (TrEMBLrel. 19,
 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
 Nature 409:685-690(2001).
EMBL: AK018515; BAB31250.1;
HSSP; P35222; '1G3J.
 PRELIMINARY;
 PRELIMINARY;
 NCBI_TaxID=7719;
 CIBETA-CATENIN.
 BETA-CATENIN.
 BETA-CATENIN.
 52. : ...
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 SEQUENCE FROM N.A.

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STRAIN=C57BL/6J; TISSUE=COLON;

XX RAWAI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Xawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alawaw K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alawaw K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Chriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Gustincich S., Hill D., Hofmann M., Hung D.A., Kamiya M., Lee N. H.,

Lyons P., Marchionni L., Mashima J., Mazazerlli J., Mombaerts P.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 SEQUENCE FROM N.A.
MEDLINE-96122902; PubMed-8562427;
Kelly G.M., Erezyilmaz D.F., Moon R.T.;
Kally G.M., Erezyilmaz D.F., Moon R.T.;
Induction of a secondary embryonic axis in zebrafish occurs following the overexpression of beta-catenin.";
Mech. Dev. 53:261-273(1995).
Mesh. V41081; AAC59732.1;
HSSP; P35222; IG3J.
 Gaps
 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterrygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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 Score 238; DB 13; Length 780;
Pred. No. 2.5e-24;
1; Mismatches 0; Indels
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01-50N-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE COLON CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:9030417H18, FULL INSERT SEQUENCE.
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
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InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 12.
SMART; SM00185; ARM; ID.
BPROSITE; PS50176; ARM REPERT; 8.
SEQUENCE 780 AA; 85542 MW; D7A1FB80F94066DC CRC64;
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Last annotation update)
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 780 AA
 Created)
 PRT;
 PRT;
 Query Match 98.8%;
Best Local Similarity 97.8%;
Matches 45; Conservative 1
 (TrEMBLrel. 01, C
(TrEMBLrel. 01, I
(TrEMBLrel. 19, I
 PRELIMINARY;
 PRELIMINARY;
 (TrEMBLrel.
 Mus musculus (Mouse).
 01-NOV-1996
01-DEC-2001
 01-NOV-1996
 B-CATENIN.
 090335
 090424
 CTNNB
 RESULT
Q9D335
 RESULT
Q90424
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 Ciona savignyi.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; Ciona.
NCBI_TaxID=51511;
 Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
Cionidae; C<u>io</u>na.
 Gaps
 Gaps
 [1].
SEQUENCE FROM N.A.
Imal K., Takada N., Satoh N., Satou Y.;
Imal K., Takada N., Satoh N., Satou Y.;
An essential role of beta-catenin in the endoderm specification of ascidian embryo.";
Princtional annotation of a full-length mouse cDNA collection.";
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 Ouery Match
Best Local Similarity 95.7%; Pred. No. 1.2e-23;
Matches 44; Conservative 0; Mismatches 2; Indels (
 Score 216; DB 5; Length 769;
Pred. No. 2.7e-21;
2; Mismatches 3; Indels
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Ozawa M., Nuruki K., Toyoyama H., Ohi Y.; "Cloning of an alternative form of plakoglobin (gamma-catenin) lacking the fourth armadillo repeat.";
 SEQUENCE FROM N.A.
MEDLINE-89264555; PubMed-2726765;
Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,
Schiller D.L., Cowin P.;
"Molecular cloning and amino acid sequence of human plakoglobin, the common junctional plaque protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989).
 MEDLINE=99386700; PubMed=10456847;
MEDLINE=99386700; PubMed=10456847;
Cerda J., Reidenbach S., Pratzel S., Franke W.W.;
"Cadherin-catenin complexes during zebrafish oogenesis: heterotypic junctions between cocytes and follicle cells.";
Biol. Reprod. 61:692-704 (1999).
EMBL; AF099738; AAD56592.1; -.
 Brachydanio rerio: (Zebrafish) (Zebra danio).
Wakaryota: Metazoa: Chordata: Cranlata: Vertebrata: Buteleostoml;
Actinopterygii: Neopterygii; Teosterygii; Teosterygii: Cyprinidae; Cyprinidae; Danio.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Māmmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Whittock N.V., Eady R.A.J., McGrath J.A.; "Genomic Organization and amplification of the human plakoglobin
 Length 729;
 Zimbelmann R.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 8.
91E00417B4FD8CEE CRC64;
 Last sequence update)
Last annotation update)
 ;
 DB 13;
 Score 190; DB 13
Pred. No. 1e-17;
 745 AA
 6; Mismatches
 Created)
 PRT;
CELL-ADHESION PROTEIN PLAKOGLOBIN.
 MEDLINE=96157724; PubMed=8576101;
 ZFIN; ZDB-GENE-991207-22; jup.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMART; SM00185; ARW; 8.
 Exp. Dermatol. 9:323-326(2000)
 PROSITE; PS50176; ARM_REPEAT; SEQUENCE 729 AA; 80033 MW;
 Biochem. 118:836-840(1995).
 SECUENCE OF 239-409 FROM N.A.
 Query Match 78.8%;
Best Local Similarity 73.9%;
Matches 34; Conservative (
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17, PLAKOGLOBIN.
 PRELIMINARY;
 Homo sapiens (Human).
 SECUENCE FROM N.A.
 HSSP; Q02248; 1DOW
 SEQUENCE FROM N.A.
 NCBI_TaxID=7955;
 NCBI_TaxID=9606;
 TISSUE-PLACENTA;
 PubMed=11016852;
 015151; 015093;
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 Gaps
 Miller J.R., McClay D.R.; "Changes in the pattern of adherens junction-associated beta-catenin accompany morphogenesis in the sea urchin embryo."; Dev. Biol. 192:310-222(1997).
 Gaps
 Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
 MEDLINE-98443204; PubMed-9769178;
Yoshida S., Marikawa Y., Satoh N.;
"Regulation of the trunk-tail patterning in the ascidian embryo: a
possible interaction of cascades between lithium/beta-catenin and
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 83.8%; Score 202; DB 5; Length 821;
82.6%; Pred. No. 2.5e-19;
iive 3; Mismatches 5; Indels
 Length 773;
 Score 216; DB 5; Length 77
Pred. No. 2.7e-21;
2; Mismatches 3; Indels
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 7.
C1340CF82AFEBDAB CRC64;
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 71E21D562A99C5AD CRC64;
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 Created)
Last sequence update)
Last annotation update)
 PROSITE; PSOU687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
PROSITE; PSS0176; ARM REPEAT; 8.
SEQUENCE 821 AA; 89558 WW; 71E21D562A99C5AD C
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 729 AA
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Pfam: PF00514; Armadillo_seg; 12.
SWART; SM00185; ARM: 12.
 PRT;
 PRT;
 SEQUENCE FROM N.A.
MEDLINE=98104237; PubMed=9441670;
 localized maternal factor pem.";
Dev. Biol. 202:264-279(1998).
EMBL. AB012160; BAA32789:1;
HSSP: P35222; 1G3J.
InterPro; IPR000225; Armadillo.
 Pfam; PF00514; Armadillo_seg; 11
SMART; SM00185; ARM; 9.
 773 AA; 85217 MW;
 PROSITE; PS50176; ARM_REPEAT;
 89.6%;
89.1%;
 (TrEMBLrel. 13, CTrEMBLrel. 13, ICTEMBLrel. 19, ICTEMBLREL.
 Ouery Match
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Watches 41; Conservative
 EMBL; U34814; AAC06340.1;
HSSP; Q02248; 1DOW.
 Conservative
 PRELIMINARY;
 PRELIMINARY;
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Matches 38; Conserv
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 BETA-CATENIN
 01-MAY-2000
01-DEC-2001
 01-MAY-2000
 SEQUENCE
 Q9PVF7
 061229
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RESULT Q9PVF7

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ð qq RESULT 061229

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Umekita Y., Liao S.;
"Molecular cloning and sequencing of the rat plakoglobin cDNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
 SEĞÜLENCE FROM N.A.
STRAIN-WILDTYPE 105;
MEDLINE-96257271; PubMed-8654977;
Hobmayer E., Hatta M., Fischer R., Fujisawa T., Holstein T.W.,
 Query Match (178.8%; Score 190; DB 11; Length 745; Best Local Similarity 73.9%; Pred. No. 1e-17; Matches 4: Thank
 Score 188; DB 5; Length 806;
Pred. No. 2.1e-17;
6; Mismatches 6; Indels
 (F1) RHOBAEMAQNAVELHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46 (F1) RHOBAEMAQNAVELHYGLPVVKLLHPPSHWPLIKATVGLIRNLGL 578 (S33 RHPDAEHAENGVRLHYGLPLVKLLNPPSRWPLIKAVVGLIRNLGL 578
 Hilparka K.A.; " " " the EMBL/GenBank/DDBJ databases. Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. EMBL; USB856; AAB06317.1; " Hispr. (200248). 2007... " " EMBL/GenBank/DDBJ databases. Diterpro: IPRO00225; Armadillo. Pfam: PPO014; Armadillo. Seg. 11. SARY: SMO0185; ARM: BPRAT; SMO0185; ARM: BPRAT; 7. SEGUES. PSS-0176; ARM: REPEAR; 7. SEGUES. PSS-0176; ARM: REPEAR; 7. SEGUES. PSS-0176; ARM: REPEAR; 7. SEGUES. PSS-0164; ARM: REPEAR; 7. SEGUES. REPEAR; 7. SEGUES. PSS-0164; ARM: REPEAR; 7. SEGUES. REPEAR; 7. S
 465; RHPEAEMAQNSVENYGIPAIVKLINOPNOMPLVKATIGLIRNLAL 510
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Pfam; PP00514; Armadillo_seg; 10.
SMARY; SM00185; ARM; 10.
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 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 Sugiyama T.;
"Identification of a Hydra homologue of the beta-catenin/lakoglobin/armadillo gene family.";
Gene 172:155-159(1996).
EMBL. 'U36781; AAC47137.1;
HSSP: Q002248; 2BCT.
 806 AA
 6; Mismatches
 678
 STRAIN-SPRAGUE-DAWLEY; TISSUE-VAGINA; Hilpakka R.A. M. G. Submitted
 STRAIN-SPRAGUE-DAWLEY; TISSUE-VAGINA;
 PRT;
 PRT;
 73.98;
 Hydra magnipapillata (Hydra).
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Matches: 34; Conservative
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NCBI_TaxID=10116;
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 BETA-CATENIN.
 Query! Match
 044326
 RESULT 12;
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ID 044326
AC 044326;
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 pLAKOGLOBIN.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Rattus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 Gaps
 Gaps
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 78.8%; Score 190; DB 4; Length 745; 73.9%; Pred. No. 1e-17; vative 8; Mismatches 4; Indels
 Length 745;
 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC000441; AAH00441.1; -.
HSSP; Q02248; 2BCT.
 4; Indels
 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
 Last sequence update)
Last annotation update)
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 Created)
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
 PRT;
 PRT;
 268228; CAA92522.1; -.
D50808; BAA0435.1; -.
A73306723; AAG16727.1; -.
AF233882; AAG16727.1; JOINED.
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01-FEB-1997 (TEMBLEEL: 02,
01-DEC-2001 (TEMBLEEL: 19,
 34; Conservative
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Best Local Similarity
Matches 34; Conserv
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 Q9BWC4;
 RESULT 10
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RX SEQUENCE FROM N.A...

RX SEQUENCE TEXAL N.A...

RX STAIN-ATCC 35092 / DSW 1617 / P2;

RX MEDLINE-21332296; PubMed-11427726;

RA Awayez M.J., Chan-Weiher C.C. f., Clausen I.G., Curtis B.A.,

RA Awayez M.J., Chan-Weiher C.C. fordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi.Ryoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 Gaps
 Gaps
 Lee.J.S., Kang H.S.; "Sequence analysis of 65G3 cosmid clone of 2ymomonas mobilis 2M4
 Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.NCBL_TaxID=2287;
 Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 Ή,
 ;
 Length 1181;
 25.1%; Score 60.5; DB 2; Length 107; 34.1%; Pred. No. 0.96; ive 7; Mismatches 15; Indels
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 containing rrnA operon.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF088097; AAF18291.1;
InterPro; IRR03844; UPF0060.
Pfam; PF02694; UPF0060; 1.
 11 protein.
107 AA; 11921 MW; 80AD302AC5926272 CRC64;
 5 AEMAQNAVRLHYGLPVVVKLL-----HPPSHWPLIKATVGLI 41
 52 AENAGKAYAVYGGIYIIMSLLWSWKVEATPPEHWDLIGAAFCLV 95
 01-WAY-2000 (TFEMBLE). 13, Last sequence update) 01-2UN-2001 (TFEMBLE). 17, Last annotation update) HYPOTHERICAL 11.9 KDA PROTEIN.
 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL GTP BINDING PROTEIN SSO2385.
 11;
 DB 5;
 938 AVRVEKGLPVLVELIRLPEDF-VVCAVATALRNLAI 972
 11. AVRLHYGLEVVVKLLHPPSHWPLIKATVGLIRNLAL 46
 351 AA
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Best Local Similarity, 141.7%, Pred. No. 5,
Matches 15, Conservative 9, Mismatches
 01 MAY-2000 (TrEMBLrel. 13, Created)
 01-OCT-2001 (TrEMBLrel. 18, Created)
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InterPro; IPR004095; TGS.
Pfam; PF02824; TGS; 1.
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 Sulfolobus solfataricus.
 -
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 STRAIN=ZM4;
 Zymomonas
 SECUENCE
 29.8H13
098H13;
098H13;
 097W55
 RESULT 14
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 Gaps
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 1;
 32.6%; Score 78.5; DB 5; Length 678; 43.5%; Pred. No. 0.023;
 "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1999).
EMBL, ALI10479; CAB60320.1; -. InterPro; IPR000225; Armadillo.
InterPro; IPR003962; FNIII_repeat.
InterPro; IPR003962; FNIII_repeat.
Pfam; PF0014; Armadillo_seg; 5.
 18; Indels
 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016853; AAB94552.1; -.
EMBL; 281564; CAB04572.1; -.
HSSP; P35222; 1G3J.
 1181 AA; 130132 MW; 4C7E23F08D34358C CRC64;
 STRAIN=N2 BRISTOL;
Costa M., Raich W., Agbunag C., Hardin J., Priess J.R.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
 McMurray A.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
 Pfan; PF00514; Armadillo_seg; 6.
PROSITE; PS50176; ARM_REPEAT; 1.
SEQUENCE 678 AA; 74510 MW; E6C7ED51F6241232 CRC64;
 1 RHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLAL 46
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 7; Mismatches
 PRT; 1181 AA.
 SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
 PRINTS; PR00014; FNTYPEIII.
SMART; SM00185; ARM; 4.
SMART; SM00060; FN3; 4.
PROSITE; PS50176; ARM_REPEAT; 2.
 InterPro; IPR000225; Armadillo.
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19,
 (TrEMBLrel, 13, (TrEMBLrel, 13, (TrEMBLrel, 19,
 Query Match 32.65
Best Local Similarity 43.55
Matches 20; Conservative
01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
 PRELIMINARY;
 Caenorhabditis elegans.
 Caenorhabditis elegans.
 Y105C5B.21 PROTEIN.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 HMP-2 OR K05C4.6
 NCBI_TaxID=6239;
 McMurray A.A.
 01-MAY-2000 (
01-MAY-2000 (
01-DEC-2001 (
 Repeat.
SEQUENCE
 Harris B
 Q9U308
 13
 RESULT
 090308
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Hypothetical protein; Complete proteome. SEQUENCE 351 AA; 39916 MW; 046A96BF004865DE CRC64; SQ

Gaps 1; Query Match

24.7%; Score 59.5; DB 17; Length 351;
Best Local Similarity 54.2%; Pred. No. 4.8;
Matches 13; Conservative 5; Mismatches 5; Indels 1;

1;

20 VVVKLLHPPSHWPLIKATVGLIRN 43 | ::|::| | | | | :||||| 120 VQIQLVNPPKSLPLSK-TIGLIRN 142

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